

1 CCATTCCAAA CAAGTCAGGA AAGCCTGCAC AGGACTGGAT AAATAATTAA
 51 GAACAGAGTG TTCTGAACAT CAACACAAAG TGGAAGAACCC TTAAGCTGAA
 101 GGTACAGTAT ATTATTACA CTGAAGGGC TTGTGTGTGG ACAAGAAAGC
 151 GCTGACAGCT CAAATGGATC CCATGGAAC GAGAAATGTC AACATCGAAC
 201 CAGATGATGA GAGCAGCAGT GGAGAAAGTG CTCCAGATAG CTACATCAGG
 251 ATAGGAAATT CAGAAAAGGC AGCAATGAGC AGTCAATTG CTAATGAAGA
 301 CACTGAAAGT CAGAAATTCC TGACAAATGG ATTTTGGGG AAAAGAAGC
 351 TGGCAGATTA TGCTGATGAA CACCATCCCCG GAACCACCTC CTTTGGATG
 401 TCTTCATTAA ACCTGAGTAA TGCCATCATG GGCAGTGGGA TCCTGGGCTT
 451 GTCCATGCC ATGGCCTACA CAGGGGTCTAT ACTTTTATA ATCATGCTGC
 501 TTGCTGTGGC AATATTATCA CTGTATTCTAG TTCACCTTT ATTAAAAACA
 551 GCCAAGGAAG GAGGGCTTT GATTTATGAA AAATTAGGAG AAAAGGCATT
 601 TGATGGCCG GGAAAATTG GAGCTTTGT TTCCATTACA ATGCAGAACCA
 651 TTGGAGCAAT GTCAAGCTAC CTCTTATCA TTAAATATGA ACTACCTGAA
 701 GTAATCAGAG CATTGATGGG ACTTGAAGAA AATACTGGAG AATGGTACCT
 751 CAATGGCAAC TACCTCATCA TATTTGTGTC TGTTGGAATT ATTCTTCAC
 801 TTTCGCTCCT TAAAAATTAA GGTTATCTTG GCTATACCAAG TGGATTTCT
 851 CTTACCTGCA TGGTGTCTT TGTTAGTGTG GTGATTTACA AGAAATTCCA
 901 AATACCTGC CCTCTACCTG TTTGGATCA CAGTGTGGA AATCTGTATC
 951 TCAACAACAC GCTTCCAATG CATGTGGAA TGTTACCCAA CAACTCTGAG
 1001 AGTTCTGATG TGAACCTCAT GATGGATTAC ACCCACCGCA ATCCTGCAGG
 1051 GCTGGATGAG AACCAAGCCA AGGGCTCTCT TCATGACAGT GGAGTAGAAT
 1101 ATGAAGCTCA TAGTGTGAC AAGTGTGAAC CCAAATACTT TGTATTCAAC
 1151 TCCCGGACGG CCTATGCAAT TCCTATCCTA GTATTGCTT TTGTATGCCA
 1201 CCCTGAGGTC CTTCCCATCT ACAGTGAAC TAAAGATCGG TCCCAGGAGAA
 1251 AAATGCAAAC GGTGTCAAAT ATTTCCATCA CGGGGATGCT TGTGATGTAC
 1301 CTGCTTGCCG CCCTCTTGG TTACCTAACCT TTCTATGGAG AAGTTGAAGA
 1351 TGAATTACTT CATGCTACA GCAAAGTGTAC TACATTAGAC ATCCCTCTTC
 1401 TCATGGTTCG CCTGGCAGTC CTTGTGGCAG TAACACAAAC TGTGCCATT
 1451 GTCTCTTCC CAATTGCTAC ATCACTGATC ACACGTGTTAT TTCCCAAACG
 1501 ACCCTTCAGC TGGATACGAC ATTTCTGAT TGCACTGTG CTTATTGCAC
 1551 TTAATAATGT TCTGGTCATC CTTGTGCCAA CTATAAAATA CATCTTCGGA
 1601 TTCACTAGGGG CTTCTCTGC CACTATGCTG ATTTTATTCT TTCCAGCAGT
 1651 TTTTATCTT AAACCTGTCA AGAAAGAAC TTTAGGTCA CCCCCAAAAGG
 1701 TCGGGGCTTT AATTTCTT GTGGTTGGAA TATTCTTCAT GATTGGAAGC
 1751 ATGGCACTCA TTATAATTGA CTGGATTAT GATCCTCCAA ATTCCAAGCA
 1801 TCACTAACAC AAGGAAAAAT AC (SEQ ID NO:1)

FEATURES:

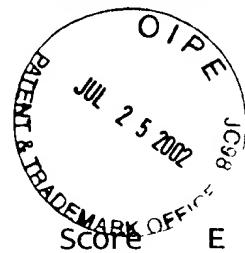
5'UTR: 1-163
 Start Codon: 164
 Stop Codon: 1805
 3'UTR: 1808

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FIGURE 1A



HOMOLOGOUS PROTEINS:

Top BLAST Hits:

			SCORE	E
CRA	145000039337444	/alt=id=gi 12017941 /def=gb AAG45335.1 AF295...	975	0.0
CRA	114000033649823	/alt=id=gi 10945621 /def=gb AAG24618.1 AF298...	597	e-169
CRA	160000003782430	/alt=id=gi 8677401 /def=gb AAF75589.2 AF1736...	591	e-168
CRA	148000002720069	/alt=id=gi 8248427 /def=gb AAF74195.1 AF2496...	587	e-166
CRA	87000000006802	/alt=id=gi 7243145 /def=dbj BAA92620.1 (AB03...	578	e-164
CRA	18000005069115	/alt=id=gi 5870893 /def=ref NP_006832.1 tran...	500	e-140
CRA	88000001154721	/alt=id=gi 7406950 /def=gb AAF61849.1 AF15985...	496	e-139
CRA	66000019404613	/alt=id=gi 9506837 /def=ref NP_061849.1 amin...	495	e-139
CRA	100000004435450	/alt=id=gi 8926332 /def=gb AAF81797.1 AF2730...	492	e-138
CRA	335001098689635	/alt=id=gi 11434147 /def=ref XP_006635.1 hy...	480	e-134

EST:

gi 10934204	/dataset=dbest /taxon=96...	1072	0.0
gi 10286121	/dataset=dbest /taxon=96...	718	0.0
gi 9872634	/dataset=dbest /taxon=960...	680	0.0
gi 2656674	/dataset=dbest /taxon=9606 ...	549	e-154
gi 9882497	/dataset=dbest /taxon=960...	541	e-151
gi 689641	/dataset=dbest /taxon=9606 /...	525	e-147

EXPRESSION INFORMATION FOR MODULATORY USE:

Library source:

Expression information from BLAST dbEST hits:

gi 10934204	whole embryo (mainly head)
gi 10286121	Hepatocellular carcinoma
gi 9872634	Non-cancerous liver
gi 2656674	Fetal liver spleen
gi 9882497	Non cancerous liver
gi 689641	Liver

Expression information from PCR-based tissue screening panels:

Mixed tissue (Brain, Heart, Kidney, Lung, Spleen, Testis, Leukocyte)

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FIGURE 1B

1 MDPMELRNNV IEPDDESSSG ESAPDSYIRI GNSEKAAMSS QFANEDTESQ
 51 KFLTNGFLGK KKLADYADEH HPGTTSGMS SFNLSNAIMG SGILGLSYAM
 101 AYTGVILFII MLLAVAILSL YSVHLLLTA KEGGSLIYEK LGEKAFGWPG
 151 KIGAFVSITM QNIGAMSSYL FIIKYELPEV IRAFMGLEEN TGEWYLNQNY
 201 LIIFVSVGII LPLSLLKNLG YLGYTSGFSL TCMFFVSW IYKKFQIPCP
 251 LPVLDHSVGN LSFNNTLPMH WMLPNNSES SDVNFMMDYT HRNPAGLDEN
 301 QAKGSLHDSG VEYEAHSDDK CEPKYFVFN RTAYAIPILV FAFVCHPEVL
 351 PIYSELKDRS RRKMQTIVSNI SITGMLVMYL LAALFGYLTG YGEVEDELLH
 401 AYSKVYTLDI PLLMVRLLAVL VAVTQTVPIV LFPIRTSVIT LLFPKRPFNW
 451 IRHFLIAAVL IALNNVLVIL VPTIKYIFGF IGASSATMLI FILPAVFYLK
 501 LVKKETFRSP QKVGALIFLV VGIFFMIGSM ALIIDWIYD PPNSKHH (SEQ ID NO:2)

FEATURES:**Functional domains and key regions:**

[1] PDO00001 PS00001 ASN_GLYCOSYLATION
 N-glycosylation site

Number of matches: 5

1	83-86	NLSN
2	260-263	NLSF
3	264-267	NNTL
4	276-279	NNSE
5	369-372	NISI

[2] PDO00004 PS00004 CAMP_PHOSPHO_SITE
 CAMP- and cGMP-dependent protein kinase phosphorylation site

503-506 KKET

[3] PDO00005 PS00005 PKC_PHOSPHO_SITE
 Protein kinase C phosphorylation site

Number of matches: 7

1	33-35	SEK
2	49-51	SQK
3	129-131	TAK
4	290-292	THR
5	360-362	SRR
6	473-475	TIK
7	506-508	TFR

[4] PDO00006 PS00006 CK2_PHOSPHO_SITE
 Casein kinase II phosphorylation site

Number of matches: 5

1	18-21	SSGE
2	22-25	SAPD
3	129-132	TAKE
4	305-308	SLHD
5	309-312	SGVE

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FIGURE 2A

Docket No.: CL001010
Serial No.: 09/776,705
Inventor: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER PROTEINS...



[5] PDO00008 PS00008 MYRISTYL
N-myristoylation site

Number of matches: 6

1	95-100	GLSYAM
2	153-158	GAFVSI
3	164-169	GAMSSY
4	186-191	GLEENT
5	296-301	GLDENQ
6	482-487	GASSAT

[6] PDO00009 PS00009 AMIDATION
Amidation site

58-61 LGKK

Membrane spanning structure and domains:

Helix	Begin	End	Score	Certainty
1	79	99	1.125	Certain
2	102	122	2.503	Certain
3	153	173	1.197	Certain
4	197	217	1.785	Certain
5	222	242	2.123	Certain
6	332	352	1.240	Certain
7	370	390	2.166	Certain
8	414	434	1.301	Certain
9	453	473	1.520	Certain
10	476	496	2.166	Certain
11	515	535	2.628	Certain

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FIGURE 2B

**BLAST Alignment to Top Hit:**

>CRA|145000039337444 /altid=gi|12017941

/def=gb|AAG45335.1|AF295535_1 (AF295535) amino acid
transport system A3 [Rattus norvegicus] /org=Rattus
norvegicus /taxon=10116 /dataset=nraa /length=547
Length = 547

Score = 975 bits (2492), Expect = 0.0

Identities = 478/547 (87%), Positives = 508/547 (92%)

Query: 1 MDPMELRNVNIEPDDDESSSGESAPDSYIRIGNSEKAAMSSQFANEDTESQKFLTNGFLGK 60
MDP+ELR+VNIEP ++S S +S Y +GNSEK AM SQFANED ESQKFLTNGFLGK

Sbjct: 1 MDPIELRSVNIEPYEDSCSVDSIQSCYTGMGNSEKGAMDSQFANEDAESQKFLTNGFLGK 60

Query: 61 KKLADYADEHHPGTTSGMSSFNLSNAIMSGILGLSYAMAYTGVILFIIMLLAVAILSL 120

K L DYADEHHPGTTSGMSSFNLSNAIMSGILGLSYAMA TG+LF+IMLL VAILSL

Sbjct: 61 KTLTDYADEHHPGTTSGMSSFNLSNAIMSGILGLSYAMANTGIVLFVIMLLTVAILSL 120

Query: 121 YSVHLLLKTAKEGGSLIYEKLGEKAFGWPKGIGAFVSITMQNIGAMSSYLFIIKYELPEV 180

YSVHLLLKTAKEGGSLIYEKLGEKAFGWPKGIGAF+SITMQNIGAMSSYLFIIKYELPEV

Sbjct: 121 YSVHLLLKTAKEGGSLIYEKLGEKAFGWPKGIGAFISITMQNIGAMSSYLFIIKYELPEV 180

Query: 181 IRAFMGLEENTGEWYLNGNYLIFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSW 240

IR FMGLEENTGEWYLNGNYL++FVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSW

Sbjct: 181 IRVFMGLEENTGEWYLNGNYLVLFVSVGIILPLSLLKNLGYLGYTSGFSLTCMVFFVSW 240

Query: 241 IYKKFQIPCPPLPVLDHSVGNLSFNNTLPMHVMLPNNSESSDVNFMDYTHRNPAGLDEN 300

IYKKFQIPCPPLPVLDH+ GNL+FNNTLPMHV+MLPNNSES+ +NFM+DYTHR+P GLDE

Sbjct: 241 IYKKFQIPCPPLPVLDHNNGNLTFNNTLPMHVIMLPNNSESTGMNFMDYTHRDP EGLDEK 300

Query: 301 QAK GSLHD SGVEYE AHSD DK CEP KY FV NS RT AY A I PI LV F AF V CH P E VL PI Y SEL KDRS 360

A G LH SGVEYE AHs D KC+PKY FV NS RT AY A I PI F AF V CH P E VL PI Y SEL KDRS

Sbjct: 301 PAAGPLHGSGVEYE AHSGDKCQPKYFV NS RT AY A I PI LAFA F V CH P E VL PI Y SEL KDRS 360

Query: 361 RRKMQTVSNISITGMLV MYLLAALFGYLTFYGEVEDELLHAYSKVYTLIDPLLMVR LAVL 420

RRKMQTVSNISITGMLV MYLLAALFGYL+FYGEVEDELLHAYSKVY D LLMVR LAVL

Sbjct: 361 RRKMQTVSNISITGMLV MYLLAALFGYLSFYGEVEDELLHAYSKVYTFDTALLMVR LAVL 420

Query: 421 VAVTQTVPIVLFPIRTSVITLLFPKRPF SWIRHFLIAAVLIALNNVLVILVPTIKYIFGF 480

VAVT TVPIVLFPIRTSVITLLFP+RPFSW+HF IAA+IALNNVLVILVPTIKYIFGF

Sbjct: 421 VAVTLTVPIVLFPIRTSVITLLFPRRPF SWKHFGIA A III A LNNVLVILVPTIKYIFGF 480

Query: 481 IGASSATMLIFILPAVFYLKLVKKETFRSPQKV GALI FLW GIFFMIGSMALIIIDWIYD 540

IGASSATMLIFILPA FYLKLVKKE RSPQK+GAL+FLV GI FM+GSMALIIIDWIY+

Sbjct: 481 IGASSATMLIFILPAAFYLKLVKKEPLRSPQKIGALVFLVTGII FMMGSMALIIIDWIYN 540

Query: 541 PPNSKHH 547

PPN HH

Sbjct: 541 PPNPDHH 547 (SEQ ID NO :4)

>CRA|114000033649823 /altid=gi|10945621

/def=gb|AAG24618.1|AF298897_1 (AF298897) amino acid
transporter system A [Homo sapiens] /org=Homo sapiens

FIGURE 2C

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/taxon=9606 /dataset=nraa /length=506
Length = 506



Score = 597 bits (1522), Expect = e-169
Identities = 315/549 (57%), Positives = 383/549 (69%), Gaps = 46/549 (8%)

Query: 1 MDPMELRVNIEPDDDESSSGESAPD---SYIRIGNSEKAAMSSQFANEDTESQKFLTNGF 57

M E+ +I PD++SSS S D SY +++AA+ S +A+ D E+Q FL

Sbjct: 1 MKKAEMGRFSISPDEDSSSYSSNSDFNYSY----PTKQAALKSHYADVDPENQNFLLESN 56

Query: 58 LGKKKLADYADEHHPGTTSFGMSFNLSNAIMGSGILGLSYAMAYTGVILFIIMLLAVAI 117

LGKKK Y E HPGTTSFGMS FNLSNAI+GSGILGLSYAMA TG+ LFI+L V+I

Sbjct: 57 LGKKK---YETEFHPGTTSFGMSVFNLNAIVGSGILGLSYAMANTGIALFIILLTFVSI 113

Query: 118 LSLYSVHLLLKTAEGGSLLIYEKLGEKAFGWPKGAFVSITMQNIGAMSSYLFIIKYEL 177

SLYSVHLLLKTA EGSSL+YE+LG KAFG GK+ A SITMQNIGAMSSYLFI+KYEL

Sbjct: 114 FSLYSVHLLLKTAEGGSLLYEQLGYKAFGLVGKLAASGSITMQNIGAMSSYLFIVKYEL 173

Query: 178 PEVIRAFMGLEENTGEWYLNGNYLIIFVSVGIIPLSLLKNLGYLGYTGFSLTCMVFFV 237

P VI+A +E+ TG WYLNNGYL++ VS+ +ILPLSL +NLGYLGYTSG SL CMFF+

Sbjct: 174 PLVIQALTNIEDKTGLWYLNNGYLVLLVSLWILPLSLFRNLGYLGYTGLSLLCMVFFL 233

Query: 238 SWIYKKFQIPCPPLPVLDHSVGNLSFNNTLPMHWMLPNNSESSDVNFMDYTHRNPAGL 297

WI KKFQ+PCP+ + N + N TL ++P

Sbjct: 234 IIVICKKFQVPCPVEAA--LIINETINTLTQPTALVP----- 269

Query: 298 DENQAK GSLHD SGVEYE AH SDDKCEPKYFV FNSRTAYA IPILVFAFVCHPEV LPIY SELK 337

+ + +D C P YF+FNS+T YA+PIL+F+FVCHP VLPIY ELK

Sbjct: 270 -----ALSHNV TENDSCRPHYFIFNSQTVYAVPILIFS FVCHPAVLPIYEELK 337

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Query: 358 DRSSRRKMQT VSNISITGMLVMYLLAALFGYLTFYGEVEDELLHAYSKVYTLIDIPLLMVRL 417

DRSRR+M VS IS M +MYLLAALFGYLTFY VE ELLH YS + DI LL+VRL

Sbjct: 318 DRSSRRRMVN VSKISFFAMFLMYLLAALFGYLTFYEHVESELLHTYSSILGTDILLIVRL 377

Query: 418 AVLVAVTQTVPIVLFPIRTSVITLLFPKRPFWSIRHFLIAAVLIALNNVLVILVPTIKYI 477

AVL+AVT TVP+V+FPIR+SV LL + FSW RH LI ++A N+LVI VPTI+ I

Sbjct: 378 AVLMAVTLTVPVWIFPIRSSVTHLLCASKDFSWWRHSLITVSILAFTNLLVIFVPTIRD 437

Query: 478 FFGFIGASSATMLIFILPAVFYLKLVKKETFRSPQKV GALIFLWG IFFMIGSMALIIIDW 537

FFFIGAS+A+MLIFILP+ FY+KLVKKE +S QK+GAL FL+ G+ M GSMALI++DW

Sbjct: 438 FFGFIGASAASMLIFILPSAFYIKLVKEPMKS VQKIGALFFLLSGVLVMTGSMALIVLDW 497

Query: 538 IYDPPNSKH 546

+++ P H

Sbjct: 498 VHNAPGGGH 506 (SEQ ID NO :5)

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF01490	Transmembrane amino acid transporter protein	187.0	2.9e-52	2
CE00398	E00398 CD53	4.0	4.8	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00398	1/1	90	110 ..	1	23	[.] 4.0	4.8

FIGURE 2D

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Docket No.: CL001010
Serial No.: 09/776,705
Inventor: Karl GUEGLER et al.
Title: ISOLATED HUMAN TRANSPORTER PROTEINS...

PF01490 1/2 99 236 .. 1 179 [. 58.9 2.5e-14
PF01490 2/2 305 529 .. 200 467 .] 133.9 3e-36



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FIGURE 2E

1 AGCTTAGCAA TATGGATCAA GAGGTCCAAT ACCTGATTAA TAAAAGTTTC
 51 AGGAGTAAAC AAAGGGGAAG AAATAGTTT TTAAATAGT AGAACTTTT
 101 TTATTTTAG AAAATGTGTC TTCTATAGAA GAAAGACAAG CCTTTTGATT
 151 GGGCGTCTG CATGCTGAGT ATGATGAATT TTAAAAGCGA CTCACATCTA
 201 GTCACGTCGT GATGAAAGGA TAAGGATAAA AATTCTGAAA TCCTCAGAAA
 251 ACCATCGATA AATTATCTAT AAAGAAATAA GAGCCAGACT CATCAATAGA
 301 AGCTAGAAGA GAGAAGTTTC TTCAATATTG TGAGGAAAA TGCTTCTGAA
 351 TCTAGAATTG AAACAATTAA CAAAGTTGAG AGGAAAATA AAGAATTTC
 401 CAACATGAAG CAACTCAGAA ATTCTATTAA CAGACATAGG CTCATTGTGT
 451 GAAAAAAAGTT ATTCAAGGCA TTATTTAGC ATAATGAAA ATAAAAGTAA
 501 GAAAGAAGAT AGAATGCCGT TCAAGAAAAGT AGCAGCTGAG CAAGACTCG
 551 AGGTTGGAGG AGGAAGCCAT TCAGAATGAG AAAGAGCATA GAAAATTGC
 601 TTTCAAAGTT TTGGTAATAT AGAATTATAT TTCACTTATT ATGTTAGTCAA
 651 ATACACCCT TTGTCTTTAG GGCATACTAT TTATACAGTG ATAATACTGT
 701 AATTGCTGCT TATTGGTTT CCATGTTAG AAACAACCTA CAGGCAAGTT
 751 ATGACACTTG TTTCACAGAA CAAGATGAAA ATATTATGAT TCTCAAATTG
 801 TAAAAGTATT TTATTAACCA AAATAATTAG GAGTGTAGGA GAAGGAAGGA
 851 AAGAAAAGAAA AAGTATGCTA ATGTCCTTAT TTTTATGGG TAACCAGTCT
 901 AAAATCAGTA AACCAAGTCA AAAAGCTTT AGTGAATTAT TCAGATCTAG
 951 AATGGCTAAC TTAAAGTAAC AAGCTAAAAA CAGAAACCGT CAATAGTGGT
 1001 TGCTGCTGGG AAGTGAGACT GGTACTGTGT GAAGAATGAG GAAAACCTT
 1051 GTACTCATTT AGTGAGTTTC TTTTTTTTCTTACCCA TATGCATGTC
 1101 TTACTTCTAT TCTCTCTTAG CTTTAACCT GCTTCTTTTCA ATCTTTTATG
 1151 TATATACATT TAGGCTGCCT TATATTAATA ATAGTTTCAT TTTGTTCCCT
 1201 CCTGCTTAAA ACACTGTGTG CTATTTTTTAAATTCTGAG AACTGCTTTC
 1251 TTTATTTCTA GACAATTCTC TGCCATTATC TCTTCTGTT TTGCTCTCACC
 1301 CTAGCTCAC AATTCTCTAT ATTGGAATGA CTATCAGTGT ATATTTGAAC
 1351 TTGTAATTCT TATTTTTCC CCATTCCTCT TAACTCTTA TTTGTTTTT
 1401 TCTTTTTTA ATCTCTTCAT GCTATAATTG GAGTGTGTTT CACAGATCTG
 1451 TCTTCAATT TTATAAGTCT CCCTTCAGCT GAGTTTTTTAAATTCAAT
 1501 GATTCTATT TTTTCTTTT TTTAAGAATT CCTTTTTTG ACTCTTTTG
 1551 CAACAGCCTG TTCTCCTTT ATATTCCTT ATAATGTTT TATTCTGTGA
 1601 AAGTTATTCT TTATTTTGA ATGTTTTCTT TCAAAATGTC TTTCTTTTA
 1651 TTAATTAAAT GTAAAAGTCC CTTTAAATT GCTTTGTTAT TTGTTAGTCC
 1701 TTAGATGTGA ATTTTATCAT TTCTTGTCCT TACTGGCACT TTGCTAGTG
 1751 AGTTCCATG TGTGTCTAT ATGTTTTGTA ATTTGAGGAT GTGAACCTTT
 1801 CTCAAGTGTG AGTGGCTTT CAAAAAAGTA CTGCCATGGC ACTGGGGTGT
 1851 GGAGGTATTC CCATGTGGTA GTTTCTGTT GTCAAGAGGAA TAGCACATT
 1901 TGTGACTTCT GGAGCAATT TTATGTTAGT TTCTCTGTC AAGATTTCT
 1951 TATCAAATGG GTATTGCACA TGTCTGACCC ACACCTTCA AGAATGATAG
 2001 TGTCTCTCCT AATACGATGG TTCAACAATA ATTGAATGAA TCTAATGGTA
 2051 AGAATTTCAAG AAGAAATTAT ATCAACTACA TATAGTAGAT TCAAGGCATT
 2101 TTCAAAAAC ACAATGCCAG TCCACCCCTT TTCACATAC AATTGAGGAA
 2151 AATGAGGTCC CCAAATGTTA AATGACTTCT GCTGAGATCC AATGAATTAA
 2201 AGGCAGAGCA GAGGCTAAAAA TCTAGATCTC TTGTTGTTA AAATACATT
 2251 TAATTTGACA CAGATGATGA GTAATGCTGA CCCAGAGGTA AATCTGAAC
 2301 TTCTTTGTT ACTATTCTA ACTTTGGCTT CAGGATCCAA GTGCCTAGAA
 2351 AGTTACTTCC TAAACATTGAT CCTCACCTAT GTTGCATATT ATCAAGCATT
 2401 TGGTGGTGT AATTCTTCA TGTCCAATTAA AATTAAGCA GTAATTTCT
 2451 TTCTAGTTAT TGCTAGTAGA GACACTGGTA GATTCTGCCT TGGTAGACCT
 2501 TCCTCTGTCA ACAATTACT TTTGTCTTCC TTCTTTAA AACATGTATC
 2551 CCACTCACAA ATACCTAAAT TTCCCTGAAG ACTGCTGCCA TGTTTAAGA
 2601 TTCTTTTTT TTTCCATAGT GACTAGTAAA ACCTGCCATT TTCATTATAC
 2651 ATAGGCACTC TATAAATATC TGCTAATTAA GCAATTATTA GTAATTCCT

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FIGURE 3A



2701 TTCTTCTCTT CCATTTCTTC CTITCTTGTA TTGGGTAAAG GAACATTTCA
 2751 GGATTTGCTT ATGAAAGTT TTCAGGAGTT TCTTCTCTTC CTCCCTTTA
 2801 CAGAGAGCAT ACAAAATGTA GATGATTAT ATTACTTAT TTCACTTAAA
 2851 TAAAATTATA ATGATGTATG TTGTGTTCTG TTTGCAGAAC AGAGTGTCT
 2901 GAACATCAAC ACAAAAGTGA AGAACCTTAA GCTGAAGGTAA CAGTATATTA
 2951 TTACACTGA AGGGGCTTGT GTGTGGACAA GAAAGCGCTG ACAGCTCAA
 3001 TGATCCCCAT GGAAGTGA AATGTCAACA TCGAACCCAGA TGATGAGAGC
 3051 AGCAGTGGAG AAAGTGTCTCC AGATAGCTAC ATCGGGATAG GAAATTCTAGA
 3101 AAAGGAGCA ATGAGCAGGT ATGGGGTTAA AAATTACTAT GTTCCATGGA
 3151 AAAATAAGAC AGGATGTGA CATGGAAAAC AGGGTCTTGA TGGGAAGAAC
 3201 TGATTTATT ACAGGTAAT TTGTGATAAC AATGATATTG ATGCTAGCAC
 3251 ATCAATTCCC TGGTCTGAA ATACAGTGTAT AATGTCATC TCTTTGTGA
 3301 CTGATTTAGA ATTGAGGTTA CAATGTCCTT GTCTCCATTA ATAATGTGTA
 3351 ATAATTTAA TTATTTAGC CTATTGCTCC TCTTATCTT CTCAGATTCC
 3401 TCTTGAATG TTGCTACACC TCCTGGTTTC TGAGGGATT CTTTCTCTC
 3451 TAAAAGTATC CTCTGGCAA GCTCACTCAC AACTACTATG GCCTCACCT
 3501 CCAAATATAT GCCATATACC CAGCCTGTTA AGTTTCTCTA CTGAATTCTA
 3551 GATAATTATA TCTGAATGTC TACTGCACGT CTCTACTGGA CCATTACTGT
 3601 GTCTAAATTG CCTCATTTAT AAAGTAAAC CTGTAATGTC TAATACTGAA
 3651 CTCTATCTT TCCCTCCAAA ACCTGCTCTT CCTCTAGTAA TCCCCATCCT
 3701 AGTAAAATC ACTGCTATCA TGAGCAACT CACTCAAAAG CCCCTAGGTG
 3751 TAAACTTGA CCCACATAGC CAACGGTCAG TCATATCCAG TTGGTTTGAC
 3801 CTTATTAATG CTTCAAATAC ACCTACTTTT CTGACCCAT TCTACTGTGG
 3851 TCTTACGTTA GGCCTACATT AAATGTGAGA CAGGGAGAGA GCCCTGATTT
 3901 CTCTCCCTGT CTTACATTTT GCTCTCCCT GTCTAGCCCT CTACACTCCT
 3951 GCAAGAGCAA TCTCTTACAA TTGCAAATTG AATCAATTTC CATCCTTAGA
 4001 TAAAGCCCTT CTGCACCTCT CCAATAGCCA TAAGAGAAAG TAGATTACAC
 4051 AACTGCTGG GCACGTAAGG TCTTTGTGA TCTGTTCTT ACCTGCCCT
 4101 CCTGCTCTGT TTTTGCCTT CTCCCTATTT GTTACTTGTG GCCTTCACTC
 4151 ATTCTGCTCC AACTGCCTGG AATCACTCAC CTGCTCCCCC TTTCTCCGTG
 4201 TTGACACCTC TCATCCTCA AGAATCAGCT CAACATCAGG TCTCCTATGC
 4251 AGCCTTTCC AAATTACTCT ACTCCCCAT GTAGAAGTGA CTGCCCTCC
 4301 TTCAATGTAAC CTCTCCCTGT GCAGATGTTA ATTACGCCAC TACTACAGGT
 4351 TAATGGCCTC TGTGGTCCCA CCACCTGCCA CATTGTCCTGG TGCAAGTGA
 4401 GTGCACAATA GTTATTGAT AAGTCAATTG ATTTCCCACA AAATGTTATA
 4451 TCAAATTGTA CATGATTAA GATGCTCAGA AGGAAATTG TGACCAAATC
 4501 TAGGCGTGAATAGAGAATA TTGTGCTCAA ACAAAAGACTT CTCATTTAT
 4551 TTACAACACC CAGGAAAATC CATCAGGAGA AACTACCGTT CTTCCCTCAA
 4601 GTAGCTCAGT GCAATGAACT TTAGGGATGT CGGACTAGAG AGGCCACTGA
 4651 GATGTAATTATC ATAGCATTTC CTAAATTAGG TGACCCCTGA AGAAACACTA
 4701 GGGTGTAGA AGACAGGGCT TTGGAGTCTG CAGAGTAGTT GCCTGACTTT
 4751 AGAGAAGCTG TTTGCTCTCT TTGAGCTTCA ATGAAAATG TAAAATGGCA
 4801 AACCAACAGC TGCTTTCAA GGATGAGATG GGTGACCCAGA ATATAGATGA
 4851 CATTCAATAC TTTTTTATTA CTTCTCCTTC ACTGCATTAC CCTCAGTAAA
 4901 TTGATTCAA CCTGAGGATG TTTCTGAAAG GCATGCACAC AAATATGAGC
 4951 TCTGCCGAGG TTGACAGAGT TAAAGGGGAC ACCCTCTAA GAACTGTCAT
 5001 AGTGTCTTC CACTTGTATCC TCAAAAGCCA GAGTAGAAAG AGCATGAATG
 5051 CTTTCTTAA GCTTCATGCA ATGTGTTCCG AACCACCTCAC AGTGAATTAC
 5101 CTTTCTTAACTC CTGGCTTAA CATAGGACAT CATTTCGAG TTTTTAAAAT
 5151 CAGTTAAAG AGATGGGTTT TATCTATGTG TGGTTGGAT TGACCCCTTA
 5201 AATGTAATTATTTT GAGAAAT TCAACATAAT GTATTTATTT GTGATCATTAA
 5251 TACTTGTGTT TTCAATACAT GCTGGGTTTG GTATCAAAAC ATTTAACATA
 5301 CTGGGGACAT TTCTCATCTA TTTTATACAA TCTTGGCATG TTAAATGACT
 5351 ACAACTCATC TCATGCCAAA ATAAGAACAT GCAAATGCCT CAAAGAAAGA

FIGURE 3B

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5401 AAATCTGTTT ACTTTCAAAT TCTCAATTAA AAAAACTACT ATGGAATACA
 5451 GATTTTAGTT TATTGATTAA AATAAAGATT CCAGAGTTTA AATTCTAGGT
 5501 GGCACTTTTG TTTTATAGT CCTCAGGCC ATTTAGGCT TCATTTATC
 5551 CTGTCACTC AGTCTCCAAC TGTGAACATT ATGTACCAAGT CTTCACATAG
 5601 CAGGTACATT AATTACAGAC CATTAAATGTA AACCCACAAAA GAGTGGTGGG
 5651 CAGTGGGTGG GGGGTGAATG GAAATGGAAA GAGGCAACAA CTGAGGGCAT
 5701 TGTGCTTCT GTGAGAAATA TGGGGAGAAG GCTAGGAAAT GTTCTTAAC
 5751 TGTGTACTCA GAGCTATTAA TGCCCTTGAGT TCTAGAAAAG CACATACAAC
 5801 TTTGTGGTTT CGTGTGCTGT TTCTATCTAC ATCTCATACT GTTTCTTATT
 5851 CTCAAAAAGT AACCCGTCA TCCTCTTTC TCTCCAGATT ATTTTCAGGA
 5901 TTAGCTCTG TTATAAAAAA TAGCTTGTAC AGATCTCCTA CAATAATTAT
 5951 TTCTATTTT ATTCTAAGG TTTATTTATT TATTATTGA GACAGACAGA
 6001 GTTCACTCT TGTGGCCCAT GCTGGAGTGC AATGGTGAA TCTCGGCTCA
 6051 CTGCAACCTC TGCCCTCCAG GTTCAAGCGA TTCTCCGT TCAGCCTCCT
 6101 GAGTAGCTGG GATTACAGGC GCCTGCCACC ACACCTGGCT AACTTTTGT
 6151 ATTCTAGTA GAGACGAAGT TTCACCATGT TGGCCAGGCT GGTCTTGAAC
 6201 TCCTGACCTC AAGTTATCCA CCCACCTCAG CCTCCCAAAG TGCTGGGATT
 6251 ACAGGCGTGA GCCACTGTGC CTGGCCTCTA GGATTATATT AATAGAACAA
 6301 TCTTCAATTAA TTTTATCTTT CTTTATCTTT CTTTTCATGT AGGAAATGTC
 6351 CTAAAATTTT CAAACCTCA ATTTGAAAGC ACTTTAAAAA TCATACATAG
 6401 TCGAGCATT TATATAAAAA CAACTAAAAA GTCTGTGACA TTTTGCAGTA
 6451 TAAAAATGCA ATGGCAGCAG CAGGCCCTAT TAATTGAGCC TCTTGGAAAT
 6501 GTGGCTGGTC CTAGGCCGT AGCCTCAAAG GCCCTGGCTT GTAATGCA
 6551 GAGCTGACCA GCACAGCTCT ATAACCAAGT TGACATCTT CTAGCCTGTG
 6601 TCCAAGAAAA CCAGAACATCAC AACGCTCTGT GGATAGTGAC ATCTTAAAGT
 6651 TTTCTTCCC TCCCAACTCT TTTGCCAGTT CATTGAATTG CTTTAATAAT
 6701 TTCTTAGTT TCATTCTTA TCTGTTAATA ATCCATGTAC ATTTTGAGAG
 6751 TAATTAAAAC ACATACGCAC ACACAGAAAC AACCAACACA ACACACAGCT
 6801 ACCACTGAAT TACTTCCAG TAAGAGATGT ATGTATAAT GATTGTACCA
 6851 AAAAAAAAAA AAGAAAGAAA ATACCAGCTA CAGGGCCCTG CCTGGGACTG
 6901 CTTGATGCCA GGGGGAGAAT GGGGTCTCCC CCTGGGTATG GGTGGGTATG
 6951 GGCCCTGCTGC TTCACCTTC TGAGCCACAG TTCCCTATAG GGATATTTG
 7001 AACATCAGAT GAGATAAGGA TCACAGTGC TAGGCATTTA ATAAATATTC
 7051 GTTGAATTAA TAAAATCATC TGATTATGGT ATGGTAGTAG TTCAGAAAAT
 7101 TCTGTATAA CCCTGTACTC TTTCTTGGA AGGGCTCTAA ATGGGAACAC
 7151 AATTAGTTGT AGTCTCTTGC ATAGCTAATG TGAGAAAGAG GGAATGTGGT
 7201 ATAAACAATT TTTTAACCAA AAATAATATT TCCTTCCTT ATAACATCCT
 7251 TCTCCATCC CAAAGTATAG TTGAAATGG AACTCAAAT TGTGGTCTG
 7301 GAATGACCGT TAGTGTGAAG GAGGAAAAGA AAATTGGGT GTCTTATTT
 7351 CCCTCCTCTG ATTCACTTAC TTAGATCACC TGAAACATAC ATATGATTCA
 7401 GAGCATATAT TTAGATGTTT TCACTTTCTT ATTTGTGTGT GTGTGTGTC
 7451 AGTCAATTG CTAATGAAGA CACTGAAAGT CAGAAATTCC TGACAAATGG
 7501 ATTTTGGGG AAAAAGAAGC TGGCAGATTA TGCTGATGAA CACGTAAGTG
 7551 AATCTATGCT TTCAGGAAT AAACGGGACT GAGGGTGTCT GATCTACCTA
 7601 GGTCTCTGTG GGAAAACAAT GTGACTGAAA TTTTCCAAGC CTTGATCAGC
 7651 ACATTCTGTG TTTATTCAAG CTCTTACTGG AATAAGGGCT TGTTTTTCC
 7701 TGTTCGCCAT ATGGCTGCAT GAATCATTAA TGAAACTTAT GTGTTTTGGG
 7751 GGGAAATCAT TCTAACCCAA AGGTAATCTA CAATCATAACA TGTTTCCCT
 7801 TCTTTATGTG ACTCCCCCTG TAATTGTAT TTTTACTGAG GCCTCTGCTG
 7851 AAACCAAGCA CTGCATTCCG TTGAAAATTA CATGCTTTTA TTGATGTTGA
 7901 GTAATGGCTT TACTCCTGTA ATGTTATCTT AGTCTTCAAT TTTGGACTGT
 7951 AATCTGCGAGA TAATGTGAGA ATAAGGATAA CCCCTAAAGG TATGCCCTT
 8001 GGCAAATGTT TGCTTATAAT ACATCCCTTC TTTTCAAGC ATCCCGAAC
 8051 CACTTCCTT GGAATGTCTT CATTAAACCT GAGTAATGCC ATCATGGCA

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FIGURE 3C

8101 GTGGGATCCT GGGCTTGTCC TATGCCATGG CCAACACAGG GATCATACTT
 8151 TTATGTAAAG TGAATGTATA TGTCTACATT TGGTGATGAA GTCCATGCAT
 8201 ACCTGGTGGC TTTTCATT AACAATCTCA AGTTTGATCT TTGTCACGT
 8251 GAAGACTCAG AGGAGGCTAA TCATGGCACT TGGTCACCCA ACCATCCCTA
 8301 ACCAACCGGC AGAAAGTGT A TGTGCTCAAT CAACCAAAGT GCTGGAGCAG
 8351 CCTCGCCAGA AGAATTTGT TATTCAAG ATACTTGAAA TAATTTGGTG
 8401 TTAGCAACC AAAAGATCT TTCCCAGAAG CAAATCTGAT TTTATCTCAT
 8451 TCTTAGGAAA GAAGCAACCA AGCCTAAGAG CCCTGCATGC CTTGCCTAC
 8501 CTTATGTCCC ATTCCCTGTA CCCCTGTGCG ACAGATACAC TGGGCACAAT
 8551 AGCCTTCTCT CCATCCTATG AAGATGCCAC ATTCCCTCTC ACCATTGGAC
 8601 CTTTGACAT GGTCTGGAA CCCTCTCTC TTCCCTCTC ATCTAGTTAA
 8651 CTCTCATAT GTCAGTTCAG TCTCACCTGA ATACTGCGCG CCCTGATCTC
 8701 CATGACTGGG GCAAATCACC TTATCATAAC ACTCACCACA ATTTTAATGT
 8751 TTAGTGCCA TTGCTCTGAT TCATTTGGTT AATATCTGTC CCTCTTGCTG
 8801 GACTATAAGC TCTAGAAAGT TGAGCCCATG TCTGTTTTA CTCACCAATG
 8851 TCTCTACCTC CAAACCTAGA GCAGTGCCTG GTACAGGCAA TATTGTTGA
 8901 GTGACCAAAC CTTATTCCTA AACCTACGTA CTTTCACCAA ACTTGTCAA
 8951 ATGCTGCCTA AGGGTAGCAG CATCTGGTAG TTGACCTGTA GGGTGGATAC
 9001 TGACTGTCT ATGACAGACA ACAACAGACG TTATGTGCA TCATGTACAG
 9051 CCTGGCATTT TCCAGGATAT AGTTGGCAGC AGTGGATTTC TTCACAAGAA
 9101 TAAAGTCTGA TGTTAGGCAC CACTGTGGAC ACAGATCCTA ATCCCAAATG
 9151 CAACGCTAGA GAGTAAATA ACTGTCTAAG AATGCAACAT TTATATCACA
 9201 AATATGTGCT GTTATGTTC TGAATATCAC ATATGATTAG TAATCACACA
 9251 GCTATTTGAG GGCTAAGCAT CAGGACTATA AATATTTGTA TTGTTAGT
 9301 GCTTTGATTG AACTCTTTA TGTATAATAT TCTTCAGCTG AATGGGTTT
 9351 TATATCAACT TTACTTTAT ATAAGCCATG TTTGAAATA AACTAGGATT
 9401 TTAATAATCT GAATTTAAT AGCTATGTAT GTAGTCATAT ATTTGTATGC
 9451 TTGTTGAATG TGCTTACCTC TAAGACAAAA AAACCTGCCT TTCCCTTATTA
 9501 ATTATACATA CCATTAATTA GAATTAGGAA GTTACAGATC ACTGATGAAT
 9551 AGAAATAGGA AAAACTCCCC CCAATCCAC AGTCATAGAT CATCTTCATG
 9601 AGAGAAGAAT GTTCCACTTT TAAAATGAG GGCCTCATTT TAGGTTATA
 9651 AACACTTAGC AGATGAATTG GGTCAAGACA ATAAATCAC TAAACATCAT
 9701 GGGGTGTGTT TTGTTGTCT AAGTAGCCCA GACTGGATTAG CTTAGTCTCT
 9751 CTTAATTAT AGCAAGTGAC ACAGTATTT AAAGGTTTTA CTCTTAGTAT
 9801 TTGTTGCCAG AGAAAGTACA TGTTTAAAGT ACAGGGAATG CTCATTATTT
 9851 TTCCAGGGAA CAAAATTATA TAATCTGAAT TACATTATTCT CTTAAAACA
 9901 GTTAAGTCA TAAGGCATAT GGAAAATAT AGGAATAAGT CATTGGTTAG
 9951 ACAGTTCTGG CAAACATACT CTATGGAAAA TAAGAGTGCAC ACATAGCTAC
 10001 AGGGGTATAA AAATTTATAA TTGTTGTCC AAATGTACAT TTGTTAGTATT
 10051 GATTTCATTG GGAATTACCA AGGGATTAGA TCAATTGTGG GGAAAGTGTAA
 10101 TTTTTAAAAA ATAAACAAAG ATAAAGATT TTTTCTGAA TTCCAGTAA
 10151 AAGGCAGCAT TGCTCCTCCA TTTATTACGT AGATGTTCT ATCAACATTC
 10201 TTATTTTGT GCTCCAAATC TTGGATTGG AAAAATACCA ATCCGTATAA
 10251 ACATAAAAGAA ACCATACATG CATGTGGGG A TCCTAACACC AGAAATGACT
 10301 CTGAATGCAA AAAAAAAAAA AAAAAAAAAA GGGAAATTTTC GTGCCCATC
 10351 CTTAGCTTTC TCTGCTTCT CTATTATATA TGCAACTGCC TGCCCTCTA
 10401 TCTTACAAAG TACTTCGAA TCTAATGCAC AGGATCAGCA GTAATGCAGC
 10451 TCAGACTGCA TGCTTTCGCC TTTGGATTCC TAGATTCAG ATTAAGGTTT
 10501 AGTCAGGCTA TTGAATAGCC CTTCAATTCT AAGTGCTGAT GTGAATATCA
 10551 TGCAAAATATG ATGTACATAT TCCCATGTGC TGAGTAAGTA GATGTAGCAT
 10601 TTGCTAATGT TGCTATACAT TTGAGCATCTA AGTTATGAAC CAGATTCTAC
 10651 CACTGGTAA CATTAAAAAA AAGTTAGGGA CTTCAAGGTAT GTAAAATATA
 10701 GCAAATTCTA TTGCTACGAC TTGAAAGGGT ATGTGTAGAG TTCTGAAAAG
 10751 AATTTCTCAG CCTCCCCAA ATCCACATAC TTTGGAAAG CTGATGATTG

FIGURE 3D

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10801 AAAAGATTAA TGTGATCCCTT TATTGTAACA TCTAACATAA TTACATTTA
 10851 TTTATTGAG AAACTTATT ACCTACTCTC TCTTCCCTT GCAGAACAT
 10901 GCTGCTTGCT GTGGCAATAT TATCACTGTA TTCAGTCAC CTTTATTAA
 10951 AAACAGCCAA GGAAGGAGGT ATGCTACCAC TTGAGTCAA CACATTCTAT
 11001 TTTAATTCTC ATAAAAGAGT ATTCAGTCT GTGCTTCAT AACCTTAGGA
 11051 TGATTATAGT CAGTTTCACA TTTCATTTTC TTCTGAGCCC AGTGACACGA
 11101 TCTCTCAGTG TTTATAGTTG TTTGGGCAAG TGAGAGGCAG GAGTGAAGT
 11151 CAACTGGCTC AGGTCAAGA CAAATAGAAA AAAGAAATTG CTGATATATG
 11201 ATAGAAATAA CTGTTTGAC TTGCTACATG CAGCTAAAAT AAATAAAACC
 11251 ATTGATTCTT GTTGGAGAA CATTTGATA TATTGCTTAT TGGTTTTGA
 11301 GGTGCTCAT TTTGGCTTA TAATTTCTAT ATGATGTTA TTTACATGTT
 11351 TGAGACTCCA GCATGGAATT ATATGACAAA AATATTTAG TCATTAAAAC
 11401 AATCTCTTTA ACAAGGCTAT TTATCTTG ATTGTAGGGT CTTGATTAA
 11451 TGAAAAATTAA GGAGAAAAGG CATTGGATG GCCGGGAAAA ATTGGAGCTT
 11501 TTGTTTCCAT TACAATGCAG AACATTGGAG GTAAGGGAT ATACTTTCA
 11551 ATGGATCCCA TAAACTTCT ATAGCGTGT CAATAAATAA GAAAACCTTAT
 11601 GGCATAAAC AGGCACTTTA GATACAGAAA AATTGCTACT TATAGTTCTT
 11651 AAATTTAAA ATGATAGTTT CTTAAATAGG TTTGTGCTCT GCTTTAATTAA
 11701 AAAACAGCAA TATCTAAGAA TGAAATAACA TATAAAACCC TGCCAATTGA
 11751 ATTCTAGAAT TAAAATATAA AATAAAAGCT TTCTTGATT TTAATGTTAT
 11801 TATAGCATGA ATTATTACTC TTTAAATGT AAGAATTGTT GCTTATATCT
 11851 GTCATTGACA AAACAGTTGA CGTTTCTAT GTGTGACTGA GTTCGATTAA
 11901 CTAACATGAA AAGTGGGTGT CTGGGGGAAC ATAGCCAAAT GCTGTGGTCC
 11951 TTGAAACGCA GCCTGCCTG AGCCAGCCCA CTAGACAGTG TCTCTGAAG
 12001 TTTACTAAGG CAAAAGCTG GCTAGGCATC AAATGCACTA TAAACCCCGG
 12051 TTTGTTGATT CTATGGATT TTATAATTCC CACTGAATTA TCATTTCCAG
 12101 TGAGGACCT AGAAATATAT ATATATATT TTAACAAATGT TCTCTCGTTG
 12151 GTGTGTTGC CCACCAAGCTT CATACTGTTT CTGGTGTGTC TTTGCCCTC
 12201 AGAAGGCATC CAAACCCATA TTTCAGATGT CCTGCCGGCT GCTTCCTGGC
 12251 ACATGGCCCC AGCCATCTCC CCACATAATG ACACCTACTC CCTCACCTCC
 12301 TACCCAGTCC CTAAACCTGC TATTCTATT CTCTGATCTT TCTTTCTCA
 12351 GTGAATACCA CCAGCAGTCA TCCAGTTCT GAGGGCAGAA ATCTGGATGT
 12401 CAGCGTAAAT GTTCTTTT CCCCAACTCT GCATGTCCAA TCAAATGGCA
 12451 AAGTCTGTC ATTGATCTC TTACTTATCT CTTGAACCTC TCCTCTCTGT
 12501 CCGCCTCAT GACCACAGAT GATCACCATT TATAGCTAG ACTATTGAG
 12551 TAGTCTCTA ACTGGTCTTC CTGGCTTGAG TTTCCCTGC TCTCAGATAA
 12601 ACTCTAATT TTTCTCCAGA TAAACTTCT CAAATTTGAG TCTGTTCTA
 12651 CTTTGTGCGT GCATAAAATT CTTCAGCATG CCTTTATTAT TTTCAAGGAA
 12701 AAACCTAAAC TCATTGGACT GACACAAGAT CTTCGTCTAG TTCTTCTGCT
 12751 CAATCTTCT AAACTTCTC AGCAATGCC ATATCTATCT ATCTTTATCT
 12801 ATCTATCTAT CTATCTATCT ATCTATCTAT CTATCTATCT ATCATCTATC
 12851 AATTTATCCA TCATCTATAC CCTACATGTC CTGTGTCAAA CCATAACAAA
 12901 TTATATTCTT TCCCCTAACCA GTACTATTAA AATATTTTA AAAATCATCC
 12951 ATGCCCTCTT TTACAGGGCT ACTTTCTCCC CTTGACTGTC TCTCAAAGTC
 13001 CTCCAACCCCT AACACACACG CACACACACA CACACACACA CACACACACA
 13051 CACACACATT TTCTCTCTA CTCTGTCAC CTGGCTTATT GCTCCTCTAG
 13101 ACTGGTAAAT ACTAGTTCTT CTGGGCTCTC ATGGTCTGT TTGTATCTAG
 13151 TATGTTACTG TTTCTAAAG GATATTAA AACACCTGAG TAGAGAATAA
 13201 GCTTTGGAG TCTGATGGAC CTGAATTGAA GTCTGTTCT GTCACATATCT
 13251 GTGAACCTGG GAAGATCACT GTACTCTTT GTCTGATTTT TTCAATGTATA
 13301 AAAATTACCT TACAAAGGCT ATTGTGAGGA TGAAATAAGG TAACATATGG
 13351 CACATAATAA GTGTTCTGTA TATGCTCTC TCCTCCCTGG TTCTCTGCTT
 13401 CCATATCCAT GTCTCTGGAG TTGCTGAAT TATTTTTAA ATAGGCATTT
 13451 AAAAATTAT AAAACAAATA TATGATGATT GTGAAAAACT AAAACACTGC



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FIGURE 3E



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13501 ATAAATATAT AAATTACCAA GAAAAGTTA TGTCAGTCAT CCTCAGAAAT
 13551 AACTACTCAT AGGTTTCCC CTATGCCTAA TTCAACAAAT ACATTGAATA
 13601 TTGTTAGTAT TGGATCATCT TATGATACCG ATTTTCAGCT TTCTTTTAA
 13651 ATTTAACAAAT ATGCCTTGAA TATATTTGCA TGTTATTCTT TTTAATGATT
 13701 TTTGAGGTTC CCATTACACA AATGTGCCAT AATTGTTTA CAGTATCCTT
 13751 ATTGATGAAC AGTTGGATTG TTTCTAATT TTCAGTGTAA TAAAAATGCT
 13801 ACAGTAAATA CACTTGCACA GAGATCTTGC AAACAGGCAA CCCATTTAA
 13851 TAAATAAATT CACTGGAGTT ATCAAGGATT TCTGGAATGC AGAAATTCT
 13901 TTAGTAATCT ATCTAACTAT ACTCACCCCTG ATAATGGATA GTGGTAAGC
 13951 AGATAAGTAA AATTCAAGCA TATCTTATGA TTGTGTTAA AAAAATTCTT
 14001 ATATGTTAAG ACTACAATCT TGGGTAGAAT TTGACAGTAA TATCAAAATT
 14051 GTCTCATTCA TTTTACTGGT TTGGAGCCAT ATGCATATT GCCCCCCAAA
 14101 TCCAACAAA TAGACCACTT TACATTTGTT TCAAACCTCTC AGCCTTATCA
 14151 AGGTTAAAG TATCGAGCAT TTCACTAGGAT TGCCCTATAG TTGGTCTAAT
 14201 TTAACAACCTG AAATAACCG GCATAAGCAT AATTAAACCT GGACTCAAGA
 14251 AGTTGAGTGG CAGCACCTCA GCTGTGGTTC AAAGCATAGC CACTACTACG
 14301 CTTCTAAACA ATGGAATAAA GTATAAAGCG GTCTCTCAGT CAAGCCTCAC
 14351 ACAGGTAAAG GGCCTGACTT TAAGGGAGTA AGATGAAATA TCGTAACATC
 14401 ACCCCAGAAA TAATGCTCTC ACTTTGGTTA CTTTATTGAA TTAGTTGATA
 14451 TTTGGATCAA GAGAAATCAC TTGTATTTCT CTATTTAACAA ACTCTACATT
 14501 TAGAACACTT AATTTCCTCA ATCCCCCTAA AAATTAACAT TTACTGCAGA
 14551 TGTGTTCAAA TTAACAGATT AATGTCCTGGA TCATTCTGAA TTTTGAGAAG
 14601 CCAAACATGT TAACATCACT GACATCACTG AAAACCAGCA ATTAATAGCT
 14651 GTAACATTGA ATGGTACCTC ACCAAGCCAG CTAATCAGAA ATATCTCCTG
 14701 TGTTCACACT CTGTAAGATT TAGCTTCTG CAAGGTCTT GCAAAGATTA
 14751 ACCAAATAAT GTGTACAGAA GGTACATCCG CTATTGTAAT AACATTTCA
 14801 CTTTGACAGT ACAGAAGAAG CACCAGCCCT TCTGTTTAG ATGTAGTCCG
 14851 TCTTTTCAA GCTGTATGAT TGTGGACATG TCAACTTAAC ATCTCGAGT
 14901 TTTTATATCT TCATCAGTGG AATGAGAATA ACAACATATA TCTTGTATC
 14951 TCACAGGGTT TTTCAAGATGA TCAAATGAAG TAATGTGCAG AACTAACCAA
 15001 TGTGGGGAAAT TATTATCATC ACTGTTACTT TCATATGAAG TGAAGAAAAT
 15051 ATTTTAAAC TCAGTAGTTT AATTACAAT TTAAGTATGT GTTTAAAGT
 15101 GCCTGTTAGC AAAAATTCAAC TAGAAGGATG TAGGACACAC TTAAAGTTT
 15151 CATGAAAAT TTGTGAGTT TATTTTAAC TGAATCTTT GGCCATGTGT
 15201 CAACAAATTA ACGTTATCCT TCACCAAATG GGTGGGCTTG AAAAAGGCGT
 15251 GATGCATAAA TATTTACAGT TGTAGGCAAA ATTGTAATGT TATGTATATG
 15301 AATACATATT CATTTTTCA GGGAGAAGGC TTGTAGATT CATCAAGAAA
 15351 TCTTCACAA GAGTAGATAA TCATTCTGT ATCACTTACC TAGATGCTCA
 15401 TGAATTTTG CCACTTATA TAATTCCTTA GTAGCCAAA AGGAGAGTAA
 15451 GATGAAGAGG GGGGAAAAAA AAAACTCTT TGACAAAGAT GGAGAGAAGC
 15501 TGTCTCTCT TGTATTCTT TATCAATCCA GGAAGCTTT GGTTTGACA
 15551 ATAAGTGGTC TGAGACTTTG TGACTCCTC AGATAGGTCC CGGAGGACTA
 15601 GATTGGTGCC CATCTGCAGA AAACCAGAGG GGATATATTG ACTCTGCAGA
 15651 TCTGCCCTTT GATTCTGCC TCTCTCAGCT GGCCCATGCC TTTTGTGCC
 15701 AGACTACTGC CCAAGTTATA GACACTAACAA CAGGCACACT GAGTATGGC
 15751 TATGTTGATT TATAACTAAT GAGGGCAGAA CCTTACAATC GCAGCTTCAC
 15801 TGAAAACCTT GGAGCAGGAT TTAACACAGA ATCAGCCCTG ATACTGTTAA
 15851 CAAAGGTCCA CCTGAAAGAG CTGGAAGGTC AAATGTCTAT CTTGGAAGAG
 15901 AACTTGGAAAG CAGTGCCAAA TACACAATGA CTTTTTTTC CATTGGGGGG
 15951 ATTAGATGTT CATCTTACAT ATCCCAAATG TCATAACTTG CTTGCATGTG
 16001 ACTTCAGTAC TGTCCACACC ATTAAGCTGT CACATTTCC ATTTTAGCAA
 16051 TGTCAAGCTA CCTCTTATC ATAAATATG AACTACCTGA AGTAATCAGA
 16101 GCATTCATGG GACTTGAAGA AAATACTGGG TATGTCTTAT GCTCCCTCTG
 16151 TGACATCAAG TGACTCATTCT TACTGGTCT TTTCTGATTCA TAATATCCCT

FIGURE 3F



16201 GTCTCTCACT TCTAGAGAAT GGTACCTCAA TGGCAACTAC CTCATCATAT
 16251 TTGTGTCGT TGAAATTATT CTTCCACTT CGCTCCTAA AAATTTAGGT
 16301 AAAGATATTT TCTAACTGGA AATATTTTA TTTTATTC ACATTTAAAT
 16351 AGGTTAGCTA ATTGTAGATG CCATATTAC CTTCCAAAAT GCTTCTCTA
 16401 ACTTCTAGGT TATCTGGCT ATACCAGTGG ATTTCTCTT ACCTGCATGG
 16451 TGTTTTTGT TAGTGTGGTA AGTGATGTGA TGACATGATC CTTGCAGGTT
 16501 GGTTAGCATG AGTTTTTTG TGCTAAATT AGTGCCTCA TTTTGTCAA
 16551 GCACTTCACT AATATGAAAT AGTTCTGTG TCACAAGTGA TTTTCTGTG
 16601 GACTAATTG GAGCAAAAAA AGAGCAGCTA CGATTTAAAG ATAGTTGAGG
 16651 TAGAATATCA AAGCTACTAC TAATGGTTG GTCTAGGCAC ACTGGTTATA
 16701 TATGGGAAA AAAGGAAAAC TTCAAGCAGG AACATGACAA TAATCTGGCA
 16751 TTTAGAACAG CAGAGGAGAG TCCCAGATGA GAAACAAGAA GGCTATATCC
 16801 ATATTCACAT GAATCAGCCA TTCTCTCTT CACATTCCAC CCATTAAGAG
 16851 AGGACAAGAA CAGTGGGATT AAAGAAGAAA TCCTCCCTCT TAGGCCCTG
 16901 ACAAAAGAGG GAATTCTTG CACTATCATG AATGCCAAA TTTATAAACG
 16951 ATTTCCCCAA AGAGGTAAG GAGAAGGAAA AAAAGTTTG AAGACCCATG
 17001 TCACCTTAGT TTGAAGAAAT AAGGAAATGA TCATCTTTCT CATGGAAGGG
 17051 CATGAAAGAG GGTGGGAAGG ATTCTTGAA AATATTGTCC TGTTAACTCT
 17101 AAGAGGCAGG GCTGCCAATC ACAGCTCCAA CTCTTCCCTT AGAACAGAGG
 17151 CTAGAGGAAG TTTACTTTGT CCATTAGTCT AAAAGGAATC CCTAACTGAG
 17201 TTCCCTCACC CCCCACCTA TAAGCCACAC ATATGGATTCT TTATTTCTT
 17251 GTTTTTCTC AAAAGCTGA TTTTTTTTC TTTTTAATG ACTGAGTCTA
 17301 GGTGATTAC AAGAAATTCC AAATACCTG CCCTCTACCT GTTTGGATC
 17351 ACAGTGTGG AAATCTGTCA TTCAACAACA CGCTTCAAT GCATGTGGTA
 17401 ATGTTACCA ACAACTCTGA GAGTTCTGAT GTGAACCTCA TGATGGATTA
 17451 CACCCACCGC AATCCTGCAG GGCTGGATGA GAACCAGGCC AAGGGCTCTC
 17501 TTCATGACAG TGGAGTAGAA TATGAAGCTC ATAGTGTGA CAAGTGTGAA
 17551 CCCAAATACT TTGTATTCAA CTCCCGGGTA AGTGAGCGGT CCGGGCTCT
 17601 AATGAGTACA GTTATGTGTT TTCTAAGTT TTATTCAATA AACTGAGATG
 17651 GCCTGAGATC ACCATCTATG TTGGAATGCT AAACACGTGG TGTGCTTT
 17701 GTTTTCAGA CGGCCTATGC AATTCTATC CTAGTATTG TTTTGTATG
 17751 CCACCCCTGAG GTCCTTCCA TCTACAGTGA ACTTAAAGAG TAAGGCAGCC
 17801 ATCATTTAG CATTCTAATT TGCTTTGAA TTCTGCTCAT ATGTTCAAAG
 17851 ATTCTTAAAC AGGAAACACA GTTTATAGCT TCCTCTTCAG AGAAAATATG
 17901 TACTCCATCC ACTCCTCACT AACATGCTTT AATCAGAAAG GTGGGAATCA
 17951 GCCCACCAACA GCACTACCTT ATCTTCTTTC TCTCCTTTCT CTCCACCAT
 18001 ATGGTTCAAGG GGAGGGTTCA ATGGCAGGTG GACAAGGAGT CGATGGTTGT
 18051 AATAATTG GCAGGTGTG GGAATTAAA TTTGAATTGT GTTCGGAAGA
 18101 AATGATGTCA GCTGGACTAG AAATGAAAAC ACCCATGACG ACCAAAACCT
 18151 ATGGTTAGGG GCAGCCTCGA TAAGCCAGTG ATGTCATTAA TAGTCAGCAC
 18201 CTAACCCCTG TCTAGAACAC ATTCTTACA AGAGATGTGT CAATATCTGT
 18251 CCTTTGTTGT CTTATTGTG CAATAGAGTC ACTGGCTAGA AAATCTTGT
 18301 TCTTCCAGCT GATGGTCTAT GGTCATTG TATTCTTTCT CTTTGAAGT
 18351 TGTTGATATT TGCTTGGAA CAAAGGATAT GAACTCTTA TAGCTTTT
 18401 CCTCTTCCCT TTAAGGGAGG ATATTATATA ATAATTCTCA ACTTCTTAA
 18451 TCTAGACATC AGTAACCTCA GTCTCATTTC TCACCAAATA GCAAAACCTT
 18501 CCCCATAAAT TCTGATTAC CTCATAAAA ATTTCAGAAC ACTTCAAGT
 18551 ATTGTGATGT CTTGATTAA CTTGAAAAT TACATGTAGC AGTTACTCCA
 18601 GAAGCCTGAC AATTGATCTT TGGCAGCCAG GTTCTTCTA GAATGGTTT
 18651 CAGAAGCTTT TCAGGTAGTC TGGACTCTG GCAGTAGTAC TTTGCTGACT
 18701 CTACTAGGTTT CTTTCTCTA TTTAAAGTCA TCTCATTATG AAATGCAAAA
 18751 GCTTCTATG TTAGGAGCCT GTTTCATCTT TATGTTAATT ATATTCTTAT
 18801 TCAGTGGCA AGCTTACTGA CCTACGTGAA ATAGACTGTT CCTCTTCTAG
 18851 GGAAATGATT GTTTTAAGA CTGAAGGACT AGTGTAAAG AAAATGGAA

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FIGURE 3G



18901 ATGAATCCTC ATTAGCTCTC TAAGACAAAT TAAATCAGC TATAAGTTTA
 18951 TGACTAAAT ATGTCTTCAT GATTAGCAAT ATAGATATAC TTTTTTATTA
 19001 TTATTTCAT TTTGAAAAGT GATTTTTTTTG TGAAAGTTA AAAAACAAAG
 19051 CTTGGTGTTC TTTCTTTTC CAGTCGGTCC CGGAGAAAAA TGAAACGGT
 19101 GTAAATATT TCCATCACCG GGATGCTTGT CATGTACCTG CTTGCCGCC
 19151 TCTTGGTTA CCTAACCTTC TATGGTAGGT CACTCTGAAA GTCATTCTCT
 19201 ATATGAAAT CCTTGTAGG CTGGTCCTTG ACCTGGTAG GTATGATTTT
 19251 TAAAATTGC CTTCTATAAG CATGCTCTAT AGATGACACA TATTCAATTA
 19301 ATATACTATT TTAGTTTGT CACTTGACCT GAGGAATGG GGCCTGATTC
 19351 AGCCTGGCTA ACAAGTTACA AGAATTGTG AATTAACACC TATTTTATAA
 19401 AAAATATCCC TCAACAAAAA TTATTTCTT CTAGGGATAG ATGATATTC
 19451 TCTGGCTAGA CTCCATAGTC CAACTCAGGC TACAAGTGT GAGAATGAAT
 19501 CCACTTGAT GTGATAAAGC TCCTTGTAT GAATTATTAA CTGCCACACA
 19551 AATAGCAGGG AAACCTGCCAG GTCCCTCAAGT TTGAATTTC CTCCTCTTA
 19601 CCAGTCAGT CAAATCTGGG AGCTTGGAC TTAGGTAAA ATTTCTGACA
 19651 TATCCCATTTC TATTTGTG TACTAAATGA TTCTCTAAGA AAGAGGACAT
 19701 GACAGAATTTC CCTTCAATCT AAGAATGCAC CACCAAAAAA AAGTGAAT
 19751 GGCCACATTA GATTATGCCT GCAACATTTC CTCTCTGGCA TCTTAACAGT
 19801 TCACAAAGGG AGTAGGATTG TACTCTTCC ATGAAGTGTG GCCACATAAA
 19851 CAGATTCAT GGAATCACAT ATTGACCTGG TAGCATATGT TTACATGAAT
 19901 CAGTGTATCA ATATAAAATAT ATTTTGTAT AACCTCCCTT TTAAAGTTT
 19951 TAACCTAATT TTTTCTTAC TGACTTGGTA AATTGAATTG CATGTATGAC
 20001 AAATTGTGGA GGAAAAGATT CAGGAGTAGG CCACCATTTG CTTAGGTTT
 20051 TTTTCTATTG GACTAATATT TGACTATTAA CCAAACATGT GCTTAGATT
 20101 GGGCATTAAAC TTTTGCCTGG TTGTGAAATA ATGAATGACG AGGTCAATAC
 20151 TACTGAAGGT ATTTTCACTA CTTTTGTCT GATCTTGAGG TGAAAATCCA
 20201 ACTACGCTTG ATTCCATAGA TATTTCTTG TTATTTGTG TTGGAGTCCT
 20251 GAATGAAGGT GTTTTCAAGT AGGGCTGCAT CTTCTCTTA GAGTAGTACC
 20301 CACTGGGAGA CCATCTAAAA ATTATACTAA TTATCCCTG CACGTTACTT
 20351 ATACTTATTG TAATGAGTTT CATAAGACAA GCAAAACTT GAAAGAGCCC
 20401 AAAAATATCT GTTTTGTG GGTGATGGAG TCATAGTTGT TGAGCTTGAA
 20451 AAAATGGTAG CAATCATTCA TCCTAGAGTT TACACACTGG GTTTGTAAACC
 20501 TGATCAGGA GTGGCTGCAC AGGTAGGGAC AGGGGAGGTG GTAGGCTGGG
 20551 AGAGACAATA TGTGGGGCTT GGGTCTCTCA TCCCCCTCAA CAAGAGCACC
 20601 TTGGTCTCTG TCTGATTGT AATTGCTTCT GTACAGCGGA GATAGATTAA
 20651 TCACAAATGTA AATGAGCTTG AGAGGCTCTT TATTTGTAT TATACCTTCT
 20701 GCAACGTTAT CAGCTTCAGG ACCTCTTGT TCATTTGAAT GAAGGTTGCA
 20751 TAGCTAATGA GCTCAGAGGC AAGACCAGAG GTGCCCTGGAT TCCCAGGCCT
 20801 AGGTCTTTC CTCTGTTCTG TGTTCTCTT ATAAAATGTT GCCATAAGTG
 20851 ACCTGTGCTG ATTTGACAAC ACCAAGCGGT TTCATTCTCTT TTTCTCTGTT
 20901 GTAGGAGAAG TTGAAGATGA ATTACTCAT GCCTACAGCA AAGTGTATAC
 20951 ATTAGACATC CCTCTCTCA TGTTCTGCCT GGCAGTCCTT GTGGCAGTAA
 21001 CACTAACTGT GCCCATTGTC CTCTCCCTAG TAAGTACATA AGACTTTGAT
 21051 GAAAGAAACC TACTTGACCC CATAAAATTAG TACATGTGTT CTACCTTCT
 21101 TTTGATTAA TTATAGGGTG AGTTGCAAT TGCAATGCCT GAGGATATTA
 21151 TTTTCTTATA GCATTTGAG TCACTAAAAA TTGCCATTG AATGTGTAGA
 21201 TAGAGCAAGT AGTTTCAGGT GGTATTTTTA TAGTGTAGGA AAAAATCAT
 21251 AAAACTTATT TTTAAACTCA AAGTTGAAAAA GTGGAGCTGG AGCTTCTGTC
 21301 TTGTGGATTAA GTAAAACCTGA GTAGGAGTTC ATATAACTTT GGAACCTTGA
 21351 AAGCCAAAAC CATATTAACCT TTCAAACTTT ATTAAATTC ATCACAGTTT
 21401 TGAAGGCATT TCATTTTTT TCCAGTTGT TGCTGCAA TAATATACAA
 21451 AAGTTGCCTT TTTAACCTG ATGCCTGAA GGCTAATGAA AAGGGGATTC
 21501 ATGTTAAGTA AATTATATAC CAGAAAAAAA TTGTTCAAAA AACAGTTATG
 21551 CTATCTATCA CATATCTCTC TCACACATGG CCTCTGCCAG ACTCACACCA

FIGURE 3H

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21601 GGTCACCCCCT CCCTGGCATT TGTCAATTGGT GTCAAGTTTG TCTGAGATCC
 21651 CAGAGCAGAG CTGGTAGTGA AGATTTGGGC TGTTGAGTT AAAACCA
 21701 CCTAAGGATA AACACAGGTC TTCACCCCTCC TGCCAGCTCC TGTTTATAA
 21751 AACTGAATT TACTCATTCA TTTGAGGGGG AAAAAAAATAA GTGACACAGT
 21801 AACCAGCACT GTCCTGGACA TAATGTTCCA TACAGGGCTG GCATATGAAG
 21851 ACTATTTCTA TAATGACACT GTGGTCACTT TAAATGCAGC TTGTGTGCTG
 21901 AAATATATTT TGGCACATTG CTTTTCATG AGTCATGAA ATCAGATCCG
 21951 TACTACTATG GTGGCTAATA TTTTACTCTT AAATCATGTC TTGCCTCTAA
 22001 TATATCTGAA AGTATTCAG ATGACATACA CATAGCTTTA GCCTAAAATC
 22051 AGCTCCGTCT TGGGTACAAG ACAGAAGACA ACTATAAACAA GAAGGTATAC
 22101 GATAGGGTAA AATTGCCAGG CAAACAACCT CACTGAGAAA AGGATATCTG
 22151 GAGCCCTTCTT TTTATGTGT AAAAAAAATCA CTCACTAAAT TTTGGCACAG
 22201 TGTAAAGCATT CACATCATTG TAGAATCAA GCATAAGAAA TCTGTGATGT
 22251 GCTTCTGTAT TGCTTTTATT ATATTCAAT AGTGTTCAG AGCCATGGTT
 22301 TTAAGGGATT GCCAGAATTG GCCATCGTCA CACAGACAGC TGGTAACAGT
 22351 TCAACTAGTG CAGCTCATAG CCCAACACTG AGGGCTGCAA TTATTGTCAT
 22401 GGGAAAGTAAA AGTCATTTAC TGATGAACAT TTCACCTCAG CATGGAAAAT
 22451 CCAAATCTCC CCTTAGAAAT TCTTACCCCTA TGAGGAAAT AAAGCACTGA
 22501 TATAATCTG ACCATCAGGA ACAGCAATAG TGTTAAACA TTAGATGCCA
 22551 TTAGAACCAA AATTGACCAT AAGAACAGA GTTCAGAAAA ATGACTAACT
 22601 GCTGCTTTC ATTATGTATT TCCACTCAAC ATTAGCATT ATGAAACATT
 22651 TTGCACATTA TCCTGCTCT ACCCTTGCAA TGTTACATT ATATAATCTG
 22701 TGTAAAGTGC CCACTGCCAC ACAGAGTCAT AAGTCCCTGG GACTTGGTGA
 22751 TGTGCACAGT GACTGGCACA GAGGGTGAGC TCTGTCGTGC TTGGGAAGAA
 22801 AAATGGCTTT CAAATGAATC TTGCTTGTG TTGAAATGTA TAAACTGCCT
 22851 TTTCTAGCAA AAGCATAGAC ACTCTTTCCC TTGGTGACAT GTGCTACGAA
 22901 TTCAAGCTGGG TTGAGGATCT GGGCTAAATG AACCAAACTT CCCTATACAT
 22951 GAAGGATACA CAGAGATGGT GACAGAGAGT GGTCACTTCC GTGAGTGGAT
 23001 CTCATCAAG TCCTCTGAAG CAAATTCAA TTTTTTTCT TTACTAAAAT
 23051 GATAAAAGTT GTTATTGGCG CTTTGCTTG TTTATTTCTG ATAACCTAGG
 23101 GCTCAGATTT TCAATGTGTC AAATGCTGAC TCACAGCATG GTTCTCTGA
 23151 CAGTTTATTT CATTAAAGGA ACTCTTCACC AGTAAGTTA TTTACTTGCC
 23201 TTGATATCTC CACACATTAA TAATAAAACT AACAAACCT AATCTGAATT
 23251 AAAATCTATC AGCTTTAGGC ATTATTTCTG GTTCTCTTC TTTCAACATG
 23301 GTAACGGGC TCTCTTCTT AGGAGCTTGA GAAGATATGA CTGGGGTTTG
 23351 TTTTCTCTA CTTCAATTAT TATCTTTCTT TTTTCCAATC AGGTTAGTTT
 23401 TTTCTTTTT AGTAAAGGT GCATAGTAAC TGCTTGTAGT ATTTGTTGAA
 23451 CAAGTGAATA AATGAAATGA ATTAAGGTAG TGTTTCACT AGCAGCCCAA
 23501 CATTCTTTC TCTCTTAGTA GTGGGTGGGG TATCAGTTAT GGAATGGCAC
 23551 CTCCCTCCAG AGGACTGATC ATGTCATT CAGCTTATGC TTCCCTTTAT
 23601 GCAGTAAAGT TTCCATATT CCATAAAGAA CAAGAAACCA AATAATCTA
 23651 ATGGATATAT AATGAACACA CAGATGAAAA TTTCACCTGC CATGCCTTTG
 23701 AAAAAAGATC CCTAGCTACT TGTATTTCAT CTTATAATT AAATCAGTCT
 23751 TTTCACTTAT GTTCTCTCA GATCTCCTGT TTGAAAGTGT ATATAGATAT
 23801 CAACATAGAA ATGCAGCGTA TATTGCTATC AACTGCAGTG GAGCAGTGAT
 23851 TCGTAGGTTT TCCAACATCC TTGCTTAAAG CAAACCTGCA AAATCAAAGT
 23901 GTGAGCTACG TCTAAACAAT GGGAGAGGCT TTTTTTTTT TTTTAAGAGT
 23951 TAGAACTAAG ACTCTCACTT CCTCCTGTGC CTCCACATT TTGACCTTCA
 24001 CATTGGGCCCT CTGCATCAGA ATACAGCACC CCCTAACAGG CTCCCTGTTCA
 24051 GGACTCTTTC TCTGGAAATA ACAGATGGTG TCTCTAGAGC TGCAAGAAC
 24101 CTTAATGGAA TCATTGTGGG TCAGAGGCC TGGATGGTGC TGGGGACCTC
 24151 CCTGACCCAC AGCATCTGAC CCACATTCC AGGTTCTAG CGACTTGTGT
 24201 CAGTAAAGAA AAAGGCACAT AGCTAAGTGG AAGAGCAGAT GAGGTTGGT
 24251 GGGAAATCAGC CAGTGGTCTG CCCTAGAAA GGTAAACAGA ACTGCTGGG

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FIGURE 3I

24301 GCTTTGGTC CTAGGCTCAC TACTCAGGG A GGCACTTTAA CATGGAATGA
 24351 CCAGCAAGTT TCCTTCTGA TCTTTCCAC CACCACACA AGCCTAGTAC
 24401 CTCCTCCCT CTTGCTCTG TTGCTCTT CGGAATGCA CTGAAACCA
 24451 CCTCAGTTC TGTTTGAAT TTTCTATTCT CTTATTAGA AAGAGGAAGA
 24501 AGCTTTGCA TTTACTCCAA CCGTTCTACC TATTATTCCC ATAAACTTTC
 24551 TGTGATCTCA TATCATTAGG CCAAATGTTA ATCTTCTGG GAGCCAGGAG
 24601 ACTGCTTCA CATTAGGAG CCCTGGACAT ATAGGACTGC CTCTAACTCA
 24651 CTCTAACTCA GCTTATTGAC TTGAATGCAC CTTTTAACAA AGTGACTAAA
 24701 AAACAAACTG TGACTATTCT CTGAAAATGA GCCTATATCT CATACTTATT
 24751 TATTCTGTT AACACTGTGA AACAAATTAA GTCTCTGGC ACTATGTATA
 24801 TACCATAAAA AGCTTATTG TAAGCCTACT AATTGGACCA GTTTGACAA
 24851 TATTGAATAA GCACTAATTG CAGATCATAA TGAGAATTA TAGGCTGCTG
 24901 AGGAAAACAA TATCACACCA TTTGCTTCC TCAGTTCCCT TTTCAGAATG
 24951 AGTTTCAAA TGTTCACTAA TCCAATTTT AAAATCCTTT ACAAAAGTTAT
 25001 TCTTAAACTA TTTCCAGAGA CTATCTGGTT TGTCTTCTA GAAATGAAAT
 25051 TGCCCTTCA GCCTAAACAG ATGGCCTTAA TTTTGGTGG AGGGTATGA
 25101 AAGGAATGTC ACATGAGAAA CTGCAAGCTA TTTAGCTTGA ATTTTTGTC
 25151 ATTCAATACAT GTTCAAAAT ATATTTACA TTTTCTCTT TTTAAATGAG
 25201 TTCCCATCTC TGACCTTAA GTGACTTCAG AACTAAAATT TTAAAGTGA
 25251 CATCAATCAC AGCATTCCA AAAATGTGAA CTCCTAGCTT AACCGAAGTA
 25301 TTCACTTATT GGAAAGCTGA TAGAGTAATT CCACTAAGTC CAAAAGTGT
 25351 CCTCTAAAAG ATTCCAAAGA TAAGAGTGT TTCAACTTTG TCAAGCTGTA
 25401 CAAACACAAA TGCACTCCC TCCCTCTGCC CACAGGGATC TTTATCCAGT
 25451 TACAGCAGCG TAACTTGAGC AGCTGCTGCA AACTGAGGCT CTCTTGACCC
 25501 TTGCTCTACT TATTCAGCT GCTAAAATAG GGCTGAAATC TGTCAAGGAT
 25551 CCTGAAGGGGA AGGATAAGAT TCCTACTATT CAATTTAATT TAAGCTTTA
 25601 TTCACTGCCT GCTGTGTGA CAACACTAAG CTAGAAAGTC TGAGGAATGT
 25651 TTAGATTATT AGGTCTGTGTT CCTTGCTTT CATAGATTTA CAATCTATTG
 25701 ATAGGGAGAG CTAAAAAGGA GAGAAAGAGG AAGGAGCAAA CATAAAAACG
 25751 TCAAAATTAA AAAATACCAT TTTAAAATT TATTTAAAAA TGTTAAATAC
 25801 CATGCAAAAT TAAGGAAAAC CTAGATTCTA AAAAATTCTT TTCAAAATCT
 25851 TGTGTAATC AATTCACTG TGCCCTTAA TGTCTCATCC AGTCTGATGA
 25901 GACATGTTTT GTGATCAACA AGGGTTTAC TATGTTTCTT AATTATGTGT
 25951 CTTGCTGTGTT ATCTCTTCT GACCGAGATT ATTTTTAACAA ATAAATTCTG
 26001 AAAACTAAGA AAGTGAAGC ATAAAATATT GTCTTATAAA ATACGCCAAG
 26051 GAAAAAAATGA CACTCCATT CAAATATCAA AAGTTAGCAT CAAGACTGCA
 26101 CAAGATGAAT GTACAGTCAT GTGTTGCTTA CAAATGTGGA CATATTCTGA
 26151 GAAATGCATC TTTAGGCAAT TTTGTCATTG TGCAAACACC ATAGATTGTA
 26201 CTTGCAGCCT AATTGGTGGA GCCTACTATA CACTAAGGCT ATATGGCATA
 26251 GCCTAGTACT CCTAGGCTAC AAACCTGTAC AGCATGTTAC TGTACTGAAT
 26301 AGTGGAGGTA CCTGTAACAT AATGGTAAGT ATTTGTGTCT CAAACGTAG
 26351 AAAAGCTACT GTAAAAATAC AGTATTACAA CCTTAGGGTA TCACTGTCTT
 26401 ATATGTGGTC TGTTGTTGAC CGAAATGACT ATGCTTAATA CCACTGAAC
 26451 GTACACTTAA AAATGGTTAA GATGGTAAAT TCTATGTTAT GTATGTTTA
 26501 TAATAATAAA AAAATTGAAA AAAGCATCAA CATCTTTCT GGGAAAAAAG
 26551 AAAAAGAAA AAAATGCATT AGAGTGATGA GAATATTTGA AGTAATAGAT
 26601 AAAGTCAAA ACAAAAGAAAT GATCTTGCT TTGAACCTTC TTGTTTAAGA
 26651 TTCGTACATC AGTGATCACA CTGTTATTTC CCAAACGACC CTTCAGCTGG
 26701 ATACGACATT TCCTGATTGC AGCTGCTGTT ATTGCACTTA ATAATGTTCT
 26751 GGTCACTCCTT GTGCCAACTA TAAAATACAT CTTCCGGATTG ATAGGTGAGT
 26801 TTCAAGAAAGG CTTCAATTG GTCAACCCAA ACTCACGCTT CATTAAATGA
 26851 TGACAGGGGA ACCAGTGCTG GGTCATCCAG ATCCCCGTTC TTTCTCAGGC
 26901 TCATGGATTTC CCTTTATCCC TGCGAGGCTC TGGTGATTGA GCTGCTCACT
 26951 GTCTCTTCTT CCTAACTGAC ACTGGGAGCC ACCTTATAGG TCATTAGTC

FIGURE 3J



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27001 AAGCTGCTTT TTCTGATAGA TGAGGAAACT GACCCCTATA AAAGTCAAGT
 27051 CATATACCTT GGTGTGGACC CAGGATTGG ACTTAGGTAT TAGCTCACC
 27101 ATCAGGAAAA GAGGAAGATA GATTTTACCT GCCAGAACG CTCTGATACT
 27151 ACCAGTATCA GCTAACATT GAAAGGTATC TTCAGAGGAA TAGGAGGTTG
 27201 ATTATATAAA GTGTATTATT AGTATTCCTT CATAACTGCA TGGTCTATTA
 27251 ATTTTCATTG TACTCATTGA GGGTTTACTT AAACCTTAAA CACAATCTAA
 27301 AACTTTAAA GAACCATGGG TAGGTCACTT GCAAAGTAAG AGGTGGATAG
 27351 GGTGTGTAT GAGTCAGCC ACCTTAGTAT GTATTTATAT TACTAATCCC
 27401 CTGTAATTTT GTGTAAATT CAGCCTTTG TTGCTTATTA TATGTTGCAT
 27451 ATACTTATGC AGCTTTGATG TTAGGTACAT TTTAATTGTC TCTATAAACAA
 27501 TATCTTCTAT GAATAAATAA CCAAGATGAG CTTATGTGAC TTAAGTGTGT
 27551 GTTTTAGTG CTAAGTATAG GATAGCTTA TATTGGTTT ATTTAAAGTG
 27601 TGTGCTGGCA TCTCCTTTC TAGGAACCTGC TGGGTAAGAC ATTGACCTTG
 27651 CCCTGTGTT GTCTTCTCAG GGGCTTCTTC TGCCACTATG CTGATTTTTA
 27701 TTCTCCAGC AGTTTTTAT CTTAAACTTG TCAAGAAAGA AACTTTAGG
 27751 TCACCCAAA AGTCGGGGT AAGTAAACCT TGCAATTCC CCCATTATTA
 27801 GTTGTCTTC CAACTACTTA GAATAAACTA GAAAATACAC ATAGTTAGA
 27851 AAAATGAATC AATGTACAAG AACCAAAAAT CAAAATGGG CTAGAACTTT
 27901 CTGGTAGCAG AGAAAGGGGA CATATTCCTG AAACTCAAAT GATTCTACTT
 27951 CAAATATCAA ATATCCTGTG TTGAGTCTGT CATACTGTC AAATAGTAGT
 28001 AGCCTTCCC ACAGACACAT ATGCTTCAGG CAAATAGCAG TGTCCAATAC
 28051 CAAGCTGCTG TTGTGCTATC CGTGGAAAAT CATGCAAGAA GGAATTAGGC
 28101 TCCCTAGCGG TGTTATGGAA TAATTTAAAT ATTTGGTCA TGGTTGTTAG
 28151 GTTTGCAAAG CAAAGGAAA GATGTTGCTT TTGTTTCCC TTCCATAGTA
 28201 CCTGTTGTCC CTGGTGTGGA CTAAGATCCA GAACAGAACCC ATTATCGTT
 28251 CTGTTAACCT CTTAGATAC AAAATACAGT CTTATTTAAAT TAGAGAGTAC
 28301 ATATTTCTT TCCATAAGAC TACTATAGAA ACAAAATGCTA GAAATAATTG
 28351 TTTTCCAAT AAGGAAATAT TATCTTTCAC TCCTTAATAA AGTCATGTTA
 28401 AGGCTTGAAA AGAATATTC TTACTGAATT ACTCTGAATT TTTACCTTGA
 28451 AGTCATTTAC CTTTGGGATG TTCTGGGAC TTCAGGATAA TTGGTATCA
 28501 AAAGGTCCAC CCAGCAGCTT GCTCCAAAT TTTAACTCTA TGTAGTCCGT
 28551 CTTGCTTGGA TTTTACAGC AGTGTGACCT TGGCAAATTAA CTTGCTCTGT
 28601 TTGTGACCTA TTTTCACTT GACCAATTGT GAAATGAGTA CAATTATCTC
 28651 CTAGACCCAT TCTAGTAAA AATGTTAGT TGCTGCTTTC TTATATGTTAG
 28701 GATTAGGAGG TTTAAGTATG TGATAAAAATG TAAGGCCCTCT TCTGGTGTAA
 28751 AAATGCTGAA GTATTTATA TGTTAGGTATG TACATATATC CTTATATATG
 28801 TGTTGTATA TTATATGTAT GCACACACAC ACACACATAT ATACACTTTT
 28851 TGTTGCAACA TCTATTAAGC TTTTGGTTT GTTTGCTTTA TAAAATTAGA
 28901 ATCATATCAT ATATGCTATT CTTTTTAAC CTGCTCTTT TCACCTAAAA
 28951 GATTGTAAGC ATTCTCTAGA TTATTGAATC TTTTCTGTC CCTTGATTTT
 29001 TAATAATCAC AGGGTATTCC ATCATCTGG TGACTAAAT CAATTAACCA
 29051 TTACTCCATT GTTGAACCTG TAGGTTGTAT CTCTCCACTG TATTCCCTTT
 29101 CTTCTTCAA CTAGGATTCT AAATTGACTG ATAGGTTAGG CCTGGGCATC
 29151 TGAGATATTA AGAATAATAT GGCTCAATAT ATAGATCAGA TTGCCATATT
 29201 ATGTAACAA CTAAAAAACAA AATTGTACTA AGTATGGTTT CTGTGCTCCT
 29251 AACAGAGTCT CTCTGAATTA CAGGCTTAA TTTTCCCTGT GGTTGGAATA
 29301 TTCTTCATGA TTGGAAGCAT GGCACCTATT ATAATTGACT GGATTTATGA
 29351 TCCTCCAAAT TCCAAGCATC ACTAACACAA GGAAAATAC TTTCTTTTC
 29401 TATTGGAAAT GGTTACAAGT TATACTCCAA AAGATATTG AATTATCTTG
 29451 ATTGGATGT TATTCTAGG AAATAACAGG AAGATTCCAA AGACGTTTAC
 29501 CAGTAATATC ACCAGGCACC TGCAGAAGAG GAAAATCACT GTTTTGTCA
 29551 AGGATGGTTG TGTATGTGTT TAAAATAAAA CCTGTGGTGC ACATTTCTAC
 29601 CCAGGTTTG CTAGAGCAGT GTGAGATGAT GAAGGTGTAT TTTTGCTGCT
 29651 TTACGAGCAG AATAAGGGTA ACTGCATGTA ACAATCATCA GATAGTACTC

FIGURE 3K

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29701 TTTCCCCCTGC CGTCTCCTCA TCCTGCACCC CCTAAAAAAG TACCAAACAT
 29751 TTGCAATTCTC AGAACATCAA ACAAAAATGC CCTGGTGGCA AAGCTATCAC
 29801 CATTAAATGT CTTCTCTCAG TCTTGACCCA AAGTCTCTGG TCTGTTTACT
 29851 AACAGAGGCA AAAGGCATGT CTTAGGAAC TGTTCGTGTT CTGTAAGGTA
 29901 CATGAATGGT CAAACACCAG TCTAGAGCAT CTTATTGTCA ACAGCAAAT
 29951 AATATTTTGC CCACCCCTGTT TGTGACATTG AGTTGTGACT TCTATATTCA
 30001 ATAGATTTTT GTAAATGTAA AAACATCTAT ATTTAAATGT TAAAACACTA
 30051 AATATAGAGA GGGGCTTTAT TTCATCATA GAGCAACAAC AAAAATAATG
 30101 CTTATAGCTA AACTGCCGT TCTAGAAAGC ATCTGCTTT TCATGTTATT
 30151 CCTAAATCCT CTTGTCATAC TTTTGTCAATT GAACAATGCT CTCCCTCTCG
 30201 TCTTCCATCC TCATTCAGAA TTTTAGAAG ACCACAATCG TGGAGATACA
 30251 CTACCCAGTA TTGTTTGATA CATTTTTATT TGATAAACAT TCAGTGCAGG
 30301 AAACTGTGAT TTGCTATATG TTTATGTATA TAATCTTATT CTGTTAGTCAT
 30351 CAGAATGTAA ATGTAAGGTA CATTGATT TTATTTTTA CATGTTAGT
 30401 TTTCTTTCTT CACAGTCAAA GCATTTATAT TATTGGGGT GGGGGCAGGG
 30451 AATTAAGTTG GTGGGCTCGA AAATCCATTC ATATGTATCT GTCTACAAAT
 30501 GTCTGGGGAT AATTTAAATT TGAAACCTAA GTTATATATA GTTTGGCAAT
 30551 GCTCTTCTTC AATATTTACA ATAATAGGAT GATCTACAAG AAAATAAGTT
 30601 TCTTTTGCA AATTTTATC ATACTAAAGT TGTTCCTTTA ATTTAGCATA
 30651 TCTAAAATAG GAATTAGTTC AGTTTAGCTC ACACAGGTGT TTGCTGACAT
 30701 TCATTGGCCA TTTAACACAG TGTTGAGTGG TTCTCCGTA AAGTATAAGT
 30751 GCTAACACTA CGAAGAAATG CACACGATCA TTCTGCTCA CTTCTATAAC
 30801 AAACTTACAT AAAATGGATT TAAAAATTCC TACTCACAGC CTAAAACCTC
 30851 TGAGTTCAC TACCTTTTT TCAAATCATA GTAAGATCAC TTGTGTATTT
 30901 TATATTTTAG TAAAGCCAAT TATGAAGTAC AAGTATCATA CACGTACTTT
 30951 TGAGCTACTA TTATTTGAAA AAAATCTGCC AAATAGCATC TTTAGGATAT
 31001 ATTTACATTT TCACTCATCT AAAAAGTATA CAAAAATAAA AAGTGGAAAA
 31051 AGGTATCTTC TGAATGTTCA AGAGCATCCT ATAGTGCCAA ATAATAAAGC
 31101 ACCATTTTT TCTTCATAAC CAGGATTAAT ATTCAATAT ACTGCAGGGC
 31151 AGACATACAT ATGATAGCTT GTGCTGATTA ATTTAACCCC ATTTGTAAC
 31201 AGATGAAAAT TTTATTTCT TATTTCATT ATAAGATGGC TCAATGTATT
 31251 GGGAGGCTTC TTTTTTATTA CAGAAAGTGT ATATTGGTAT ATAATAAATG
 31301 AACTTTCAA ATGACTATGA TGTGATTTT GATCTATTGT TAAAGAATGT
 31351 TGTGTTATTT GTCCATGAAA CAAAATTAA AATCCAATAA CTGCTTTCT
 31401 TATATTGGTT TATGTTCCAT TTTCATTGTT ACCTTTGACA CATAACTAAC
 31451 ATCTATAGCC ATCATCCTGA AAATAATTGC CATCTTATT TGGCAAAATA
 31501 GATATTTAAT CCTAAATTAT TATGATGATT ATAATTTGG CATCACATAT
 31551 ATACCACTA GAATGAATGT GGAAGAAATG AGTCTTTAT GGTTAGTTG
 31601 AAAGAATCCA TTGAAGATAG AAAATGAGAG AATAGAAGAA ACCTGAGAAT
 31651 AGTAAAATAA AGAGCAGAGA AAAATATGGGG GCAGGGAAAA CATGTGAGTG
 31701 CTAAGGATTG ATTATGAATG AACGATTAGG GGGATTGATG GATCACAGGG
 31751 TAAGTATATG CTTAACCTTA TAAGAAACTT CCACATAGTT TTCCACAGTG
 31801 TTTCTACCAT TTTCATTCC ACCCGTACTA CCTACAACTT CCACTGACTC
 31851 CACAGCCCTG CCAACATTG GTGTTGCTT TTGCTTTTA GCCTTTCTAG
 31901 TGGGTCTGAA ATGGTAATC ATTGTGATT TCATTTCTGC TTCTGTGACA
 31951 ACTAATGTIG AAAACTTTTC AAGTGTAA TGTCACTCA TATATCTTCT
 32001 TTTGTGAAGT GTGTATTCAA ATCTTTGCC CATTTTAAA ATTTAGGTTA
 32051 TGTGTTTTA TTGGGTATT GTAGAAGCTC TTTAAATATG GATCCATGTC
 32101 CAGATTGCCA ATATATTTTC CCAGTCTATG GTATGGTTGC TTATTTCTC
 32151 AAAGGTGTCT TAATTACATC TTTCTGGGC CAGGTCACCA TAGCTCAAAG
 32201 TTTTGCATT TATGTCTTAA TGAGATAATA TTAATCAGAG TGGTATAGTC
 32251 AAAATTAAAT GTTTGTGATGT CCTGGGCCA TATAGGTAGG ACTGGATCAT
 32301 CTAACCAAGA TGCAAAAAAA AAAAACAAAA AAAACAAAAA TAGTACTTGG
 32351 AAAACTTAT TTAAATTAA ACA (SEQ ID NO:3)



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FIGURE 3L



FEATURES:

Start: 3000
 Exon: 3000-3118
 Intron: 3119-7452
 Exon: 7453-7543
 Intron: 7544-8039
 Exon: 8040-8155
 Intron: 8156-10894
 Exon: 10895-10968
 Intron: 10969-11437
 Exon: 11438-11530
 Intron: 11531-16047
 Exon: 16048-16129
 Intron: 16130-16215
 Exon: 16216-16298
 Intron: 16299-16408
 Exon: 16409-16467
 Intron: 16468-17301
 Exon: 17302-17577
 Intron: 17578-17709
 Exon: 17710-17789
 Intron: 17790-19073
 Exon: 19074-19174
 Intron: 19175-20904
 Exon: 20905-21029
 Intron: 21030-26649
 Exon: 26650-26794
 Intron: 26795-27670
 Exon: 27671-27768
 Intron: 27769-29273
 Exon: 29274-29372
 Stop: 29373

CHROMOSOME MAP POSITION:

Chromosome 12

ALLELIC VARIANTS (SNPs):

DNA Position	Major	Minor	Domain	Protein Position	Major	Minor
1386	T	C	Beyond ORF(5')			
2594	T	C	Beyond ORF(5')			
2757	G	T	Beyond ORF(5')			
6107	C	T	Intron			
6392	T	C	Intron			
9484	C	G	Intron			
10280	A	G	Intron			
10297	G	A	Intron			
10331	G	A	Intron			
10536	T	C	Intron			
11548	T	C	Intron			
11917	G	T	Intron			
12840	T	-	Intron			
12844	A	-	Intron			

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FIGURE 3M



12847	T	-	Intron
13019	C	-	Intron
13022	A	G	Intron
13285	G	A	Intron
14461	G	C	Intron
15464	-	G	Intron
15469	-	A	Intron
15545	T	C	Intron
16199	T	C	Intron
16798	T	C	Intron
18103	C	T	Intron
18421	A	G	Intron
18528	G	A	Intron
18722	T	C	Intron
18775	C	G	Intron
18951	T	C	Intron
18974	T	G	Intron
19540	A	C	Intron
19841	G	A	Intron
20170	A	C	Intron
20343	T	C	Intron
20519	G	A	Intron
20963	T	C	Exon
21840	G	T	Intron
22783	C	T	Intron
22787	G	A	Intron
22825	T	C	Intron
22967	A	T	Intron
23248	A	G	Intron
23764	G	T	Intron
23765	C	T	Intron
24432	A	G	Intron
24538	C	G	Intron
24693	T	C	Intron
24819	C	T	Intron
25743	C	T	Intron
26044	G	C	Intron
26555	G	A	Intron
27886	A	C	Intron
31884	T	C	Beyond ORF(3')
32229	T	A	Beyond ORF(3')

411 P P

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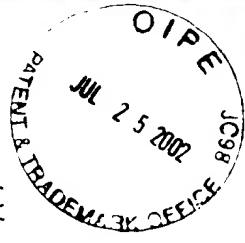
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Context:

DNA
Position
 1386

ACCCATATGCATGTCTTACTTCTATTCTCTCTAGCTTTAACCTGCTTCATCTT
 TTATGTATATACTTTAGGCTGCCCTATATTAATAATAGTTCACTTTGTTCTCCTGC
 TTAAAACACTGTGTGCTATTTAAATTCTGAGAACTGCTTTCTTATTTCTAGACAA
 TTCTCTGCCATTATCTCTTCTGTTCTCACCCTAGTCTACAATTCTCTATATTGG
 AATGACTATCAGTGTATTTGAACCTGTAATTCTATTCTTCCCCATTCTCTTAACCT
 [T, C]
 CTTATTTGTATTTCTTTTAATCTCTCATGCTATAATTGAGTGATTTCCACAGA
 TCTGCTTCAATTATAAGTCTCCTCAGTGAGTTTTAAATTCAATGATTCT

FIGURE 3N



2594

ATTTTTTCTTTTTAAAGAATTCCCTTTTGACTCTTTGCAACAGCCTGTTCTCC
TTTATATTCTTATAATGTTTATTCTGTGAAAGTTATTCTCTTATTGAATGTTT
TCTTCAAAATGCTTTATTAAATTAAATGAAAAGTCCCTTTAAATTGCTTG

SEQ ID NO: 6

CTGAACCTTCTTGTACTATTCTAACCTGGCTTCAGGATCCAAGTGCCTAGAAAGT
TACTTCTAAACTGATCCTCACCTATGTCATATTATCAAGCATTGGTGGTGTAAAT
TCTTCTATGTCATTAAGCAGTAATTCTTAGTTAGTATTGCTAGTAGAGAC
ACTGGTAGATTCTGCCTGGTAGACCTTCTGTCAACAATTACTTTGTCCTCCTT
CTTTAAAACATGTATCCCACTCACAAATACCTAAATTCTTGAAGACTGCTGCCATGT
[T, C]

TTAAGATTCTTTTCCATAGTGAAGTAGTAAACCTGCCATTTCATTATACATAG
GCACTCTATAAATATCTGCTAATTAGCAATTATTAGTAATTCTTCTTCTTCCAT
TTCTTCTTCTTGTATTGGTAAAGGAACATTCAAGGATTGCTATGTAAGTTTCA
GGAGTTTCTTCTTCCCTCCCTTACAGAGAGCATACAAATGATGATTATTC
ACTTATTCTATTAAATAATATAATGATGATGTTGTGTTCTGAGAACAGAG

SEQ ID NO: 7

2757

TTATTGCTAGTAGAGACACTGGTAGATTCTGCCTGGTAGACCTTCTGTCAACAAATT
TACTTTGCTTCTTCTTAAACATGTATCCCACTCACAAATACCTAAATTCTT
GAAGACTGCTGCCATGTTAAAGATTCTTCTTCTTCTTCAAGTAGTGAAGTAGAACTGC
CATTTCTTCTCTTCCATTCTTCTTCTTGTATTGGTAAAGGAACATTCAAGGATT
[G, T]

CTTATGTAAGTTTCAGGAGTTCTTCTTCTCCCTTTACAGAGAGCATACAAAT
GTAGATGATTCAATTCACTTATTCTTATTAAATAAAATTATAATGATGATGTTGTGTT
CTGTTGAGAACAGAGTGTCTGACATCAACACAAAGTGGAGAACCTTAAGCTGAAG
GTACAGTATATTATTACACTGAAGGGCTTGTGTGGACAAGAAAGCGCTGACAGCTC
AAATGGATCCCAGGAACTGAGAAATGTCACATCGAACAGATGATGAGAGCAGCAGTG

SEQ ID NO: 8

6107

GTTTCTGTGCTGTTCTATCTACATCTCATACTGTTCTATTCTAAAAAGTAACCCCT
GTCATCTCTTCTCTCCAGATTATTCAGGATTAGCTCTGTTATAAAAATAGCTT
GTACAGATCTCCTACAATAATTATTCTATTCTATTCTAAGGTTATTATTATTAA
TTGAGACAGACAGAGTTCACTCTGTGGCCATGCTGGAGTGAATGGTGAATCTCGG
CTCACTGCAACCTCTGCCCTCCAGTTCAAGCGATTCTCTGTGTTAGCCTCCTGAGTAG
[C, T]

TGGGATTACAGGCGCTGCCACCACACTCGGCTAACCTTTGTATTCTAGTAGAGACGA
AGTTTCAACCATGTTGGCCAGGCTGGTCTGAACTCCTGACCTCAAGTTATCCACCCACCT
CAGCCTCCAAAGTGTGGATTACAGGCGTGAGCCACTGTGCTGCCCTAGGATTAT
ATTAATAGAACAACTTCAATTATTATCTTCTTATCTTCTTCTATGTAGGAAAT
GTCCTAAATTTCAAACCTCAATTGAAAGCACTTTAAAATCATACATAGTCGAGCA

SEQ ID NO: 9

6392

CAGCCTCTGAGTAGCTGGATTACAGGCGCTGCCACCACACTCGGCTAACCTTTGTA
TTCTAGTAGAGACGAAGTTCACCATGTTGGCCAGGCTGGTCTGAACTCCTGACCTCA
AGTTATCCACCCACCTCAGCCTCCAAAGTGTGGATTACAGGCGTGAGCCACTGTGCC
TGGCCTCTAGGATTATATTAAATAGAACAACTCTCAATTATTATCTTCTTATCTTCTT
TTCTATGTTAGGAAATGTCCTAAATTGAAACCTCAATTGAAAGCACTTTAAAAT
[T, C]

ATACATAGTCGAGCATTATATAAAAACAACAAAAAGTGTGACATTGCACTATA
AAAATGCAATGGCAGCAGCAGGCTTATTAAATTGAGCTCTGGAAATGTGGCTGGTCT
AGGTCCGTAGCCTCAAAGGCCCTGGTGTAACTGCAAGGAGCTGACCAGCACAGCTAT
AACCAAGTTGTACATCTCTAGCCTGTGTCAGAAAACAGAACATACAACGCTGTGG
ATAGTGCACATCTAAAGTTCTTCCCTCCAACTCTTGCAGTTCAATTGAAATTGCT

SEQ ID NO: 10

9484

GCAACATTATACACAAATATGTGCTGTTATGTTCTGAATATCACATATGATTAGTAA
TCACACAGCTATTGAGGGCTAAGCATCAGGACTATAAAATTGTTATTGTTAGTGT

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FIGURE 30



- TTGATTGAACCTTTATGTATAATTCTTCAGCTGAATGGGTTTATATCAACTTTA
CTTTATATAAGCCATGTTTGAAATAAACTAGGATTTAATAATCTGAATTAAATAGC
TATGTATGTAGTCATATATTGTATGCTTTGAATGTGCTTACCTCTAACAGACAAAAAA
[C, G]
CTGCCCTTCCATTAAATTACATACCATAAAATGAATTAGGAAGTTACAGATCACTG
ATGAATAGAAATAGGAAAACCTCCCCAATCCCACAGTCAGATCATCTTCATGAGAG
AAGAATGTTCCACTTTAAAATGAGGGCCTCATTAGGCTTATAAACACTTAGCAGAT
GAATTGGTCAGAACAAATTAAATCACTAAACATCATGGGGTGTGTTTGTGTCTAAAG
AGCCCAGACTGGATTAAGCTTCTCTTAATTAGCAAGTGACACAGTATTTAAAG
SEQ ID NO: 11
- 10280 ATAAGAGTCAACATAGCTACAGGGGTATAAAATTATAATTACATGGTCAAATGTACA
TTTGTAGTATTGATTCTGGATTACCAAGGGATTAGATCAATTGTGGGAAAGTGT
ATTTTTAAAATAAACAAAGATAAAAGATTCTGAATTCCAGGTAAAAGGCAGCA
TTGCTCCTCCATTATTACGTAGATGCTCTATCAACATTCTTATTTTGTGCTCCAAT
CTTGGATTGGAAAAATACCAATCCGTATAAACATAAAAGAACATACATGCATGTGGGG
[A, G]
TCCTAACACCAGAAATGACTCTGAATGCAAAAAAAAAAAAAAGGAAATTTC
GTGCCCATCCTAGTTCTCTGCTTCTATTATATATGCAACTGCCGCCCTCTA
TCTTACAAAGTACTCGTAACTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCA
TGCTTCGCTTGGATTCTAGATTCAAGGTTAGTCAGGCTATTGAATAGCC
CTTCAATTCTAAGTGTGATGTGAATATCATGCAAATATGATGTACATATCCATGTGC
SEQ ID NO: 12
- 10297 CTACAGGGTTATAAAATTATAATTACATGGTCAAATGTACATTGTAGTATTGATTTC
ATTGGATTACCAAGGGATTAGATCAATTGTGGGAAAGTGTATTTTTAAAATAAAC
AAAGATAAAAGATTCTGAATTCCAGGTAAAAGGCAGCATTGCTCCCTCATTTATT
ACGTAGATGCTCTATCAACATTCTTATTTTGTGCTCCAATCTGGATTGGAAAAAT
ACCAATCCGTATAAACATAAAAGAACATACATGCATGTGGGATCTAACACCAAGAAAT
[G, A]
ACTCTGAATGCAAAAAAAAAAAAAAGGAAATTCTGTGCCCATCCTAGCT
TTCTCTGCTTCTATTATATATGCAACTGCCGCCCTCTATCTACAAAGTACTTCG
TAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCATGCTTCGCCCTTGGAT
TCCTAGATTCAAGGTTAGTCAGGCTATTGAATAGCCCTCAATTCTAAGTGT
GATGTGAATATCATGCAAATATGATGTACATATCCATGTGCTGAGTAAGTAGATGTAG
SEQ ID NO: 13
- 10331 AAATGTACATTGTAGTATTGATTCTGGATTACCAAGGGATTAGATCAATTGTGG
GGAAAGTGTATTTTAAAATAAACAAAGATAAAAGATTCTGAATTCCAGGTAA
AAGGCAGCATTGCTCCCTCATTTATTACGTAGATGCTCTATCAACATTCTTATTTGT
GCTCCAATCTGGATTGGAAAATACCAATCCGTATAAACATAAAAGAACATACATG
CATGTGGGATCTAACACCAAGAAATGACTCTGAATGCAAAAAAAAAAAAAAA
[G, A]
GGAATTCTGTGCCCATCCTAGCTTCTGCTTCTATTATATATGCAACTGCC
GCCCTCTATCTACAAAGTACTTCGTAACTAATGCACAGGATCAGCAGTAATGCAGCT
CAGACTGCATGCTTCGCCCTTGGATTCTAGATTCAAGGTTAGTCAGGCTAT
TGAATAGCCCTCAATTCTAAGTGTGATGTGAATATCATGCAAATATGATGTACATATT
CCCATGTGCTGAGTAAGTAGATGCTATTGCTATACATTAGCATCTAA
SEQ ID NO: 14
- 10536 TACCAATCCGTATAAACATAAAAGAACATACATGCATGTGGGATCTAACACCAAGAA
TGACTCTGAATGCAAAAAAAAAAAAAAGGAAATTCTGTGCCCATCCTAG
CTTCTCTGCTTCTATTATATATGCAACTGCCGCCCTCTATCTACAAAGTACTT
CGTAATCTAATGCACAGGATCAGCAGTAATGCAGCTCAGACTGCATGCTTCGCCCTTGG
ATTCCCTAGATTCAAGGTTAGTCAGGCTATTGAATAGCCCTCAATTCTAAGTGT
[T, C]
TGATGTGAATATCATGCAAATATGATGTACATATCCATGTGCTGAGTAAGTAGATGT
GCATTGCTAATGTGCTATACATTAGCATCTAAGTTATGAACCAGATTCTACCACTGG

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FIGURE 3P



11548

GTAACATTAAAAAAAGTTAGGGACTTCAGGTATGAAAATATAGCAAATTCTATTCTA
CGACTTAAAGGGTATGTAGAGTCTGAAAAGAATTCTCAGCCTCCCCAATCCAC
ATACTTTGAAAGCTGATGATTGAAAAGATTAATGTGATCCTTATTGTAACATCTAAC

SEQ ID NO: 15

ACCATTGATTCTGTTGGAGAACATTGATATATTGCTTATTGGTTTGAGGTTGCA
TCTTTGGGCTTATAATTCTATATGATGTTATTACATGTTGAGACTCCAGCATGGA
ATTATATGACAAAATATTAGTCATTAACAACTCTTTAACAGGCTATTATCT
TTGATTGAGGGCTTGTGATTGAAAATTAGGAGAAAAGGCATTGGATGCCGGGA
AAAATTGGAGCTTGTCCATTACAATGCAGAACATTGGAGTAAGGGATATACTTT
[T,C]
CAATGGATCCCATAAAACTTTCTATAGCGTGTCAATAAAATAAGAAAACCTATGGCAATAA
ACAGGGCACTTAGATACAGAAAATTGCTACTTATAGTTCTAAATTAAAATGATAGT
TTCTTAAATAGGTTGTGCTGCTTAAATTAAAACAGCAATATCTAAGAATGAAATAA
CATATAAAACCTGCCAATTGAAATTCTAGAATTAAAATAAAAAGCTTCTGAT
TTTAATGTTATTATAGCATGAATTATTACTCTTTAAATTGAAGAATTGTGCTTATAT

SEQ ID NO: 16

11917

TTTAGATACAGAAAATTGCTACTTATAGTTCTAAATTAAAATGATAGTTCTTAAA
TAGGTTTGTGCTCTGCTTAAATTAAAACAGCAATATCTAAGAATGAAATAACATATAAA
ACCTGCCAATTGAATTCTAGAATTAAAATAAAAATAAGCTTCTGATTTTAATG
TTATTATAGCATGAATTATTACTCTTTAAATTGAAGAATTGTGCTTATATCTGCTATT
GACAAAACAGTTGACGTTCTATGTGACTGAGTCGATTACTAAACTGAAAAGTGG
[G,T]
TGTCTGGGGAACATAGCCAAATGCTGTGGCTTGAAACGCAGCCTGCACTGAGCCAGC
CCACTAGACAGTGTCTCTGGAAGTTACTAAGGCAAAGTCTGGCTAGGCATCAAATGCA
CTATAAAACCCGGTTGTGATTCTATGGATTCTATAATTCCACTGAATTATCATTTC
CAGTGTAGGACCTAGAAATATATATATATTAAACAAATGTTCTCGTGGTGTGTT
TGCCCACCAAGCTTCATACTGTTCTGTTGTCTTGGCCCTCAGAAGGCATCAAACCO

SEQ ID NO: 17

12840

GACTATTGCACTAGTCTCTAACTGGCTTCCCTGGCTTGAGTTCCCTGCTCTCAGATA
AACTCTAATTGTTCTCCAGATAAAACTTCTCAAATTGAGTCTGTTCTACTTTGTCG
TGCATAAAATTCTCAGCATGCCCTTATTATTCAAGGAAAACCTAAACTCATTGGAC
TGACACAAGATCTCGTCTAGTTCTCTGCTCAATCTTCTAAACTTCTAGCAATGCC
CATATCTATCTATCTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT
[T,-]
ATCATCTATCAATTATCCATCATCTATACCCATGTCCTGTGCAAAACATAACAAA
TTATATTATTCCCTAACAGTACTATTAAATTATTAAAATCATCCATGCCCTT
TTCACAGGCTACTTTCTCCCTTGACTGTCCTCAAAGTCTCCAACCCCTAACACACACG
CACACACACACACACACACACACACACACATTTCTCTCACTCTGCTCAC
CTGGTCTATTGCTCCTAGACTGGTAAACTAGTTCCCTGGGCTCTCATGGCCTGT

SEQ ID NO: 18

12844

ATTGCACTAGTCTCTAACTGGCTTCCCTGGCTTGAGTTCCCTGCTCTCAGATAAAACT
CTAATTGTTCTCCAGATAAAACTTCTCAAATTGAGTCTGTTCTACTTTGTCGTGCA
AAAAATTCTCAGCATGCCCTTATTATTCAAGGAAAACCTAAACTCATTGGACTGAC
ACAAGATCTCGTCTAGTTCTCTGCTCAATCTTCTAAACTTCTAGCAATGCCATA
TCTATCTATCTTATCTATCTATCTATCTATCTATCTATCTATCTATCT
[A,-]
TCTATCAATTATCCATCATCTATACCCATGTCCTGTGCAAAACATAACAAAATTAT
ATTATTCCCTAACAGTACTATTAAATTATTAAAATCATCCATGCCCTTCTTCA
CAGGCTACTTTCTCCCTTGACTGTCCTCAAAGTCTCCAACCCCTAACACACACGACA
CACGACA
TCTATTGCTCCTAGACTGGTAAACTAGTTCCCTGGGCTCTCATGGCCTGT
SEQ ID NO: 19

12847

GCAGTAGTCTCTAACTGGCTTCCCTGGCTTGAGTTCCCTGCTCTCAGATAAAACTCTA
ATTGTTCTCCAGATAAAACTTCTCAAATTGAGTCTGTTCTACTTTGTCGTGCAATAA

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FIGURE 3Q

A circular stamp from the OIPE (Oficina de Patentes y Trademark Office) dated JUL 25 2002, with file number J098.

	AATTCTTCAGCATGCCTTATTATTTCAAGGAAAAACTAAACTCATTGGACTGACACA AGATCTCGTCTAGTCTCTGCTCAATCTTCAAACCTTCTAGCAATGCCATATCT ATCTATCTTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCATC [T,-]
	ATCAATTATCCATCATCTACCTACATGTCTGTCAAACCATAACAAATTATATT TATTCCCCTAACAGTACTATTTAATATTAAAATCATCCATGCCTCTTACAG GCTACTTTCTCCCCTGACTGTCTCAAAGTCCTCCAACCCTAACACACACGACACAC AC ATTGCTCTAGACTGGTAAATACTAGTCCCTGGGCTCTATGGCTCTGGTATC SEQ ID NO: 20
13019	CTGACACAAAGATCTCGTCTAGTCTCTGCTCAATCTTCAAACCTTCTAGCAATGC CCATATCTATCTATCTTATCTATCTATCTATCTATCTATCTATCTATCTATCTAT CTATCATCTATCAATTATCCATCATCTACCTACATGTCTGTCAAACCATAACA AATTATATTATTCCCCTAACAGTACTATTTAATATTAAAATCATCCATGCCTTC TTTCACAGGCTACTTCTCCCCTGACTGTCTCAAAGTCCTCCAACCCTAACACACA [C,-] GCAC CCTGGCTATTGCTCTAGACTGGTAAATACTAGTCCCTGGGCTCTATGGCTCTG TTGTATCTAGTATGTTACTGTTCTAAAGGATATTAAAACACTTGAGTAGAGAATA AGCTTTGGAGTCTGATGGACCTGAATTGAGTCTGTTCTGACTATCTGTAACCTG GGAAGATCACTGACTCCTTGTGATTTTGTATAAAAATTACCTAACAAAGGC SEQ ID NO: 21
13022	ACACAAGATCTCGTCTAGTCTCTGCTCAATCTTCAAACCTTCTAGCAATGCCA TATCTATCTATCTTATCTATCTATCTATCTATCTATCTATCTATCTATCTA TCATCTATCAATTATCCATCATCTACCTACATGTCTGTCAAACCATAACAAAT TATATTATTCCCCTAACAGTACTATTTAATATTAAAATCATCCATGCCTCTT TCACAGGCTACTTCTCCCCTGACTGTCTCAAAGTCCTCCAACCCTAACACACACGC [A,G] CAC GGTCTATTGCTCTAGACTGGTAAATACTAGTCCCTGGGCTCTATGGCTCTGTT GTATCTAGTATGTTACTGTTCTAAAGGATATTAAAACACTTGAGTAGAGAATAAGC TTTGGAGTCTGATGGACCTGAATTGAGTCTGTTCTGACTATCTGTAACCTGGG AGATCACTGACTCCTTGTGATTTTGTATAAAAATTACCTAACAAAGGCAT SEQ ID NO: 22
13285	ACTGCTCTCAAAGTCCTCCAACCCTAACACACACGACACACACACACACACAC CACACACACACACATTCTCTCACTCTCACCTGGCTATTGCTCTAGACTG GTAAATACTAGTCCCTGGGCTCTATGGCTCTGTTGTATCTAGTATGTTACTGTT CTAAAGGATATTAAAACACTTGAGTAGAGAATAAGCTTTGGAGTCTGATGGACCTGA ATTGAGTCTGTTCTGTCACTATCTGTAACCTGGGAAGATCACTGACTCCTTGTCT [G,A] ATTTTTCTATGTATAAAAATTACCTACAAAGGCTATTGAGGATGAAATAAGGTAAACA TATGGCACATAATAAGTGTCTGTATATGCTCTCTCCCTGGTCTCTGCTTCCATA TCCATGTCTGGAGTGGCTGAATTATTAAAATAGGCATTAAAAAATTATAAAAAC AAATATATGATGATTGTGAAAAACTAAAACACTGCATAAATATATAAAATTACCAAGAAAA GTTATGTCAGTCATCCTAGAAATAACTACTCATAGGTTTCCCCTATGCCATTCAA SEQ ID NO: 23
14461	TATCGAGCATTCTAGGATTGCCTTATAGTGGTCTAATTAAACAACGAAATAACCA GCATAAGCATAATTAAACCTGGACTCAAGAAGTGGAGTGGCAGCACCTCAGCTGTGGTC AAAGCATAGCCACTACTACGCTCTAAACAATGGAATAAGTATAAGCGTCTCTCAGT CAAGCCTCACACAGGTAAGAGGGGTGACTTTAAGGGAGTAAGATGAAATATCGTAACATC ACCCAGAAATAATGCTCTCACTTGGTACTTTATTGATTAGTGTATTTGGCATAAA [G,C] AGAAATCACTGTATTCTCTATTAAACAACCTACATTAGAACACTTAATTCTCAA TCCCCCTAAAAATTAAACATTACTGCAAGATGTTTACATTAACAGATTAAATGCTGGAT

FIGURE 3R

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15464

CATTCTGAATTTTGAAGACCAAAACATGTTAACATCACTGACATCACTGAAAACCAGCAA
TTAATAGCTGTAACATTGAATGGTACCTCACCAAGCCAGCTAATCAGAAATATCTCCTGT
GTTCACACTCTGTAAGATTAGCTTAGCCAAGGTCTTGCAAAGATTAACCAAATAATG

SEQ ID NO: 24

15469

TGAGTTCTATTTAACTGAATCTTGGCATGTCACAAATTAACTTACGTTATCCTTCA
CCAAATGGGTGGGCTTGAAAAAGGCGTGTGCATAAATATTACAGTTGAGGCAAATT
GTAATGTTATGTATATGAATACATATTCACTTTTCAAGGAGAAGGCTGTAGATTTCAT
CAAGAAATCTTCACAAGAGTAGATAATCATTATGTATCACTACCTAGATGCTCATGA
AATTTGCCACTTATATAATTCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGG
[-,G]

AAAAAAAAAAACTCTTTGACAAGATGGAGAGAAGCTGTCATCTCTGTATTCTTATC
AATCCAGGAAGCCTTGGTTTGACAATAAGTGGTGTGAGACTTGTACTCCTCAGAT
AGGTCCCGAGGAGTAGATTGGTGCCCCTGAGCTGGCCATGCCAGCTGAGCTGGGGATATTGACTC
TGCAGATCTGCCCTTGATTCTGCCATCTCTCAGCTGGCCATGCCCTTGTTGCCAGAC
TACTGCCAAGTTAGACACTAACACAGGCACACTGAGTATGGCTATGTTGATTATA

SEQ ID NO: 25

15545

TCTATTTAACTGAATCTTGGCATGTCACAAATTAACTTACGTTATCCTTCACAAA
TGGGTGGGCTTGAAAAAGGCGTGTGCATAAATATTACAGTTGAGGCAAATTGTAAT
GTTATGTATATGAATACATATTCACTTTTCAAGGAGAAGGCTGTAGATTTCATCAAGA
AATCTTCACAAGAGTAGATAATCATTATGTATCACTACCTAGATGCTCATGAAATT
TGCCACTTATATAATTCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGGAAAA
[-,A]

AAAAACTCTTGACAAGATGGAGAGAAGCTGTCATCTCTGTATTCTTATCAATCC
AGGAAGCCTTGGTTTGACAATAAGTGGTGTGAGACTTGTACTCCTCAGATAGGTC
CCGGAGGACTAGATTGGTGCCCCTGAGAAAACCAGAGGGGGATATTGACTCTGAG
ATCTGCCCTTGATTCTGCCATCTCTCAGCTGGCCATGCCCTTGTTGCCAGACTACTG
CCCAAGTTAGACACTAACACAGGCACACTGAGTATGGCTATGTTGATTATAACTAA

SEQ ID NO: 26

16199

AGGCCTGATGCATAAAATATTACAGTTGAGGAAAATTGTAATGTTATGTATGAATA
CATATTCACTTTTCAAGGAGAAGGCTGTAGATTCAAGAAATCTTCACAAGAGT
AGATAATCATTATGTATCACTTACCTAGATGCTCATGAAATTGCCACTTATATAAT
TCCTTAGTTAGCCAAAAGGAGAGTAAGATGAAGAGGGGGAAAAAAACTCTTGTAC
AAAGATGGAGAGAAGCTGTCATCTCTGTATTCTTATCAATCCAGGAAGCCTTGGTT
[T,C]

TGACAATAAGTGGTGTGAGACTTGTACTCCTCAGATAGGTCCCGAGGACTAGATTG
GTGCCCATCTGAGAAAACCAGAGGGGGATATTGACTCTGAGATCTGCCCTTGATTG
TGCCATCTCAGCTGGCCATGCCCTTGTTGCCAGACTACTGCCAAGTTAGACAC
TAACACAGGCACACTGAGTATGGCTATGTTGATTATAACTAATGAGGGCAGAACCTA
GAACCTGAGCTTCACTGTAACACTTGGAGCAGGATTAAACACAGAACTGCCCTGACT

SEQ ID NO: 27

16798

AGAACTTGGAAAGCAGTGCCAAATACACAATGACTTTTCCATTGGGGATTAGATG
TTCATCTTACATATCCAAATGTCATAACTTGGTGTGATGTGACTTCAGTACTGTCACA
CCATTAAGCTGTCACATTCCATTAGCAATGTCAAGTACCTCTTATCATTAAATA
TGAACCTACCTGAAGTAATCAGAGCATTGAGCTTGAAGAAAATCTGGTATGTCTT
ATGCTCCCTGTGACATCAAGTGACTCATTCTACTTGGTCTTGTGATTCTAATATCC
[T,C]

TGTCTCTCACTTCTAGAGAAATGGTACCTCAATGGCAACTACCTCATCATATTGTGCTG
TTGGAATTATTCTCCACTTGGTCTTAAATAGGTTAGCTAATTGTAGATGCCATATTCA
CCTTCCAAATGCTCTTCAACTTCTAGTTATCTGGTATACCAGTGGATTCTCT
TACCTGAGCTGGTGTGTTAGTGTGGTAAGTGATGTGACATGATCCTGCAGGT

SEQ ID NO: 28

GTTGGTTAGCATGAGTTTGTGCCAAATTAGTGTCTCATTTGTTCAAGCACTTC
ACTAATATGAAATAGTTCTGTATCACAAGTGATTCTGTAGACTAATTAGAGCAA

FIGURE 3S

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18103

AAAAGAGCAGCTACGATTTAAAGATAGTTGAGGTAGAATATCAAAGCTACTACTAATGTTGGTCTAGGCACACTGGTTATATATGGGAAAAAGGAAAACCTCAAGCAGGAACATGCAATAATCTGGCATTAGAACAGCAGAGGAGTCCCAGATGAGAAACAAGAAGGCTATA [T, C]

CCATATTACATGAATGCCATTCTCTTACACATTCCACCCATTAAAGAGAGGACAAG AACAGTGGGATTAAGAAGAAATCCTCCTCTAGGCCCTGACAAAGAGGGAATTCT TGCACTATCATGAATGCCAAAATTATAAAGCATTCCCAAAGAGGTAAAGGAGAAGGA AAAAAAGTTTGAGAGCCCAGTCACCTTAGTTGAAGAAAATAGGAAATGATCATCTT CTCATGGAAGGGATGAAAGAGGGTGGAGGATTCTTGAAAATATTGTCCTGTTAACT

SEQ ID NO: 29

18421

CATTTAGCATTCTAATTGCTTGAATTCTGTCATATGTTCAAAGATTCTTAACAG GAAACACAGTTATAGCTTCCCTCTCAGAGAAAATATGACTCCATCCACTCCTCAGTAA CATGCTTAATCAGAAAGGTGGAAATCAGCCACACAGCACTACCTTATCTCTTCTC TCCTTCTCTCCACCATAATGGTCAGGGAGGGGTTCATGGCAGGTGGACAAGGAGTCG ATGGTTGAATAATTGGCAGGTGGAAATTAAATTGAATTGTTGAAGAAA [C, T]

GATGTCAGCTGGACTAGAAATGAAAACACCCATGACGACAAAACCTATGGTAGGGCA GCCTCGATAAGCCAGTGATGTCATTATAGTCAGCACCTAACCCCTGTCTAGAACACATT CATTACAAGAGATGTGTCATAATCTGCTTGTCTTGTACAATAGACTGGCTAGAAAATCTGTT GGCTAGAAAATCTGTTCTCCAGCTGATGGTCTATGGTCATTGTATTCTTCCCT TTGAAGTTGTTGATATTGCTTGGAAACAAAGGATATGAACCTATTAGCTGTTCTCCT SEQ ID NO: 30

18528

AAATGAAAACACCCATGACGACAAAACCTATGGTAGGGCAGCCTCGATAAGCCAGTG ATGTCATTATAGTCAGCACCTAACCCCTGTCTAGAACACATTCTTACAAGAGATGTGTAATATCTGCTTGTCTTGTACAATAGACTGGCTAGAAAATCTGTT TCTTCCAGCTGATGGTCTATGGTCATTGTATTCTTCCCTTGAAGTTGTTGATATT TGCTTGGAAACAAAGGATATGAACCTATTAGCTGTTCTCTTCCCTTAAAGGAGG [A, G]

TATTATATAATAATTCTCAACCTTTAACTAGACATCAGAACCTCAGTCTTCATTCT CACTAAATAGCAAACCTTCCCCATAAAATTCTGATTTACCTCATAAAAATTCAGAACAC CTTTCAAGTATTTGATGTCCTTGATTTACTTTGAAAATTACATGTAGCAGTTACTCCAG AAGCCTGACAATTGATCTTGGCAGCCAGGTTCTTCTAGAATGGTTTCAAGCAGTTT CAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTCCCTCAT SEQ ID NO: 31

18722

ACAAGAGATGTGTCATAATCTGCTTGTCTTATTGTACAATAGACTGGCTAGGAGAAAATCTGTTCTTCCAGCTGATGGTCTATGGTCATTGTATTCTTCCCTTGA AGTTGTTGATATTGCTTGGAAACAAAGGATATGAACCTATTAGCTGTTCTCTTCTT CCTTAAAGGAGGATATTATAATAATTCTCAACCTTTAACTAGACATCAGAACCTCAGTCTT CAGTCTTCATTCTCACTAAATAGCAAACCTTCCCCATAAAATTCTGATTTACCTCATAAA [G, A]

AAATTTCAGAACACTTCAAGTATTTGATGTCCTTGATTTACTTTGAAAATTACATGTA GCAGTTACTCCAGAAGCCTGACAATTGATCTTGGCAGCCAGGTTCTTCTAGAATGGTT TTCAGAAGCTTCTAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGG TTCTTCTCTTCTCATTAAAGTCATCTCATTAGAACATGCAAAGCTTCTATGTTAGGAGC CTGTTCATTTATGTTAATTATATTCTTCTAGTGGCAAGCTTACTGACCTACGTG SEQ ID NO: 32

TATTATATAATAATTCTCAACCTTTAACTAGACATCAGAACCTCAGTCTTCATTCT CACTAAATAGCAAACCTTCCCCATAAAATTCTGATTTACCTCATAAAAATTCAGAACAC CTTTCAAGTATTTGATGTCCTTGATTTACTTTGAAAATTACATGTAGCAGTTACTCCAG AAGCCTGACAATTGATCTTGGCAGCCAGGTTCTTCTAGAATGGTTTCAAGCAGTTT CAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTCCCTCAT [T, C]

TAAAGTCATCTCATTAGAACATGCAAAGCTTCTATGTTAGGAGCCTGTTCATCTTAT GTTTAATTATATTCTTATTCTAGTGGCAAGCTTACTGACCTACGTGAAATAGACTGTTCC

FIGURE 3T

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18775

TCTTCTAGGGAAATGATTGTTTTAAGACTGAAGGACTAGTGTAAAGAAAAATGGAAAT
GAATCCTCATTAGCTCTAAGACAAATTAAATCAGCTATAAGTTATGACTAAAT
GTCTTCATGATTAGCAATATAGATATACTTTTATTATTATTTCTTTGAAAAGTGA

SEQ ID NO: 33

18951

TCATTCTCACTAAATAGCAAAACTTCCCCATAAAATTCTGATTACCTCATAAAAAATT
CAGAACACTTCAGTATTGATGTCCTTGATTACTTGAAGAAATTACATGTAGCAGTT
ACTCCAGAAGCCTGACAATTGATCTTGGCAGGCCAGGTTCTCTAGAATGGTTTCAGA
AGCTTTAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTT
TCCTCATTAAAGTCATCTCATTATGAAATGCAAAGCTTCTATGTTAGGAGCCTGTT
[C,G]

ATCTTATGTTAATTATATTCTTATTCACTGGCAAGCTACTGACCTACGTGAAATAGA
CTGTTCTCTAGGGAAATGATTGTTTAAGACTGAAGGACTAGTGTAAAGAAAAA
TGGAAATGAATCCTCATTAGCTCTAAGACAAATTAAATCAGCTATAAGTTATGTAC
TAAATATGTCATGATTAGCAATATAGATATACTTTTATTATTATTTCTTTGAA
AAAGTGATTTTTTTGTAAGTTAAAAAACAAAGCTTGGTGTCTTCTTTCCAGTC

SEQ ID NO: 34

18974

CAGAACGTTTCAGGTAGTCTGGACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTT
CTTTCTCATTAAAGTCATCTCATTATGAAATGCAAAGCTTCTATGTTAGGAGCCT
GTTTCTCTTATGTTAATTATATTCTTATTCACTGGCAAGCTACTGACCTACGTGAA
ATAGACTGTTCTCTTAGGGAAATGATTGTTTAAGACTGAAGGACTAGTGTAAAG
AAAAATGGAAATGAATCCTCATTAGCTCTAAGACAAATTAAATCAGCTATAAGTTA
[T,C]

GTACTAAATATGTCATGATTAGCAATATAGATATACTTTTATTATTATTTCTT

TTGAAAAGTGAATTGTTGTAAGTTAAAAAACAAAGCTTGGTGTCTTCTTTCC
AGTCGGTCCCAGGAAAAATGCAAACGGTGTCAAATATTCCATCACGGGGATGCTTGT
ATGTACCTGCTTGGCGCCCTCTTGGTACCTAACCTTCTATGGTAGGTCACTCTGAAAG
TCATTCTATATGCAAATCTGTTAGGCTGGCCTTGACCTGGTAGGTATGTTT

SEQ ID NO: 35

19540

ACTCCTGGCAGTAGTACTTTGCTGACTCTACTAGGTTCTTCTCATTAAAGTCATCT
CATTATGAAATGCAAAGCTTCTATGTTAGGAGCCTGTTCTATCTTATGTTAATTATA
TTCTTATTCACTGGCAAGCTTACTGACCTACGTGAAATAGACTGTTCTCTTAGGGA
AATGATTGTTTAAGACTGAAGGACTAGTGTAAAGAAAATGGAAATGAATCCTCATT
AGCTCTAAGACAAATTAAATCAGCTATAAGTTATGACTAAATATGTCATGAT
[T,G]

AGCAATATAGATATACTTTTATTATTATTTCTATTGAAAAGTGATTTTTGTA

AGTTAAAAAACAAAGCTTGGTGTCTTCTTCTCAGTCGGTCCGGAGAAAATGCA
AACGGTGTCAAATATTCCATCACGGGGATGCTTGTATGTACCTGCTTGGCGCCCTCTT
TGGTACCTAACCTCTATGGTAGGTCACTCTGAAAGTCATTCTATATGCAAATCCTT
GTTAGGCTGGCCTTGACCTGGTAGGTATGTTTAAAAATTGCCTTCTATAAGCATG

SEQ ID NO: 36

19841

GGTATGATTTAAAAATTGCCTCTATAAGCATGCTATAGATGACACATATTCAATT
AATATACTATTAGTTGTCACCTGACCTGAGGAAATGGGGCCTGATTCAAGCTGGCT
AACAGTACAAGAATTGTAATTAAACACCTATTATAAAAATATCCCTCAAACAAA
ATTATTCTCTAGGGATAGATGATATTCTCTGGCTAGACTCCATAGTCCAACTCAGG
CTACAAGTGTGAGAATGAATCCACTTGATGTGATAAGCTCCTTGATGGAATTATTA
[A,C]

CTGCCACACAAATAGCAGGGAAACTGCCAGGTCTCAAGTTGAATTGCCTCTCTTA
CCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTCAGTC
TATTGTTATACTAAATGATTCTCTAAGAAAGAGGACATGACAGAATTCTTCAATCT
AAGAATGCAACCACCAAAAAAGTGAATGGCCACATTAGATTATGCTGCAACATT
CTCTCTGGCATCTAACAGTCACAAAGGGAGTAGGATTGACTCCTCCATGAAGTGTG

SEQ ID NO: 37

FIGURE 3U

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TATTTTGTATACTAAATGATTCCTAAGAAAGAGGACATGACAGAATTCTTCAATC
AAGAACATGACCAACAAAAAAAGTGAATGGCCACATTAGATTATGCCCTGCAACATTC
CTCTCTGCATCTAACAGTTACAAAGGGAGTAGGATTGTACTCCTCCATGAAGTGTG
[G, A]

CCACATAAACAGATTCTATGGAATCACATATTGACCTGGTAGCATATGTTACATGAATC
AGTGATCAATATAAATATTTTGATAAACCTCTTAAAGTTAACTTAATT
TTTCTTACTGACTGGTAAATTGAATTGCATGTATGACAATTGAGGAAAAGATT
AGGAGTAGGCCACCATTGCTTAGGTTTTCTATTGACTAATATTGACTATTAAC
CAAACATGTGCTTAGATTGGCATTAACTTTGCCGGTGTGAAATAATGAATGACGA

SEQ ID NO: 38

20170 TATTGACCTGGTAGCATATGTTACATGAATCAGTGTATCAATATAAATATTTGTA
TAAACCTCTTAAAGTTAACTTAATTCTTACTGACTGGTAAATTGAATT
GCATGTATGACAATTGAGGAAAAGATTAGGAGTAGGCCACCATTGCTTAGGTT
TTTCTATTGACTAATATTGACTATTACCAACATGTGCTTAGATTGGCATTAA
CTTTTGCCGGTTGTGAAATAATGAATGACGAGGTCAACTACTGAAGGTATTCACT
[A, C]

CTTTTGTCTGATCTTGAGGTGAAAATCCAACACTACGCTTGATTCCATAGATATTCTTG
TTATTGCTGGAGTCCTGAATGAAGGTGTTCAAGTAGGGCTGCATCTCGCTTAA
GAGTAGTACCCACTGGGAGACCATCTAAAATTACTAATTATCCCTGCACGTTACTT
ATACTTATTAAATGAGTTCATAGACAAGCAAAACTGAAAGAGGCCAAAATATCT
GTTTAGTGTGGTGTGGAGTCATAGTTGAGCTGAGGGTAAATTGAGCTTGTGAA

SEQ ID NO: 39

20343 TAGGTTTTCTATTGACTAATATTGACTATTACCAACATGTGCTTAGATTGG
GCATTAACCTTTGCCGGTTGTGAAATAATGAATGACGAGGTCAACTACTGAAGGTAT
TTCACTACTTTGCTGATCTTGAGGTGAAAATCCAACACTACGCTTGATTCCATAGATA
TTTCTTGTATTGCTGGAGTCCTGAATGAAGGTGTTCAAGTAGGGCTGCATCT
TCGTCTAGAGTAGTACCCACTGGGAGACCATCTAAAATTACTAATTATCCCTGCA
[T, C]

GTTACTTATACTTATTAAATGAGTTCATAGACAAGCAAAACTGAAAGAGGCCAAA
AATATCTGTTAGTGTGGTGTGGAGTCATAGTTGAGCTGAGGGTAAATTGAGCTTGTGAA
TCATTCTAGAGTTACACACTGGGTTGTAACCTGCATCAGGAGTGGCTGCACAGG
TAGGGACAGGGAGGTGGTAGGCTGGAGAGACAATATGAGGGCTGGGTCTCTCATCC
CTTCAACAAGAGCACCTGGTCTCTGATTTGTAATTGCTCTGACAGGGAGAT

SEQ ID NO: 40

20519 GATATTCTTGTATTGCTGGAGTCCTGAATGAAGGTGTTCAAGTAGGGCTGC
ATCTCGCTTAGAGTAGTACCCACTGGGAGACCATCTAAAATTACTAATTATCCC
TGCACGTTACTTATACTTATTAAATGAGTTCATAGACAAGCAAAACTGAAAGAGC
CCAAAATCTGTTAGTGTGGTGTGGAGTCATAGTTGAGCTGAGGGTAAATTGGT
AGCAATCATTCTAGAGTTACACACTGGGTTGTAACCTGCATCAGGAGTGGCTGC
[G, A]

CAGGTAGGGACAGGGAGGTGGTAGGCTGGAGAGACAATATGAGGGCTGGGTCTCTC
ATCCCCTCAACAAGAGCACCTGGTCTCTGCTGATTGTAATTGCTCTGACAGGG
AGATAGATTATCACAATGAAATGAGCTGAGAGGCTCTTATTGTTGATTATACCTTC
TGCAACGTTATCAGCTTCAGGACCTTTGTCATTGAAATGAAGGTGCTAGCTAATG
AGCTCAGAGGAAGACCAAGAGGTGCCTGGATTCCAGGCCTAGGTCTTCTGTTCT

SEQ ID NO: 41

20963 TGAGCTTGAGAGGTCTTATTGTTGATTATACCTCTGCAACGTTATCAGCTTCAGGAC
CTCTTGTCTATTGAATGAAGGTGCTAGCTAATGAGCTCAGAGGAAGACCAAGAGGT
GCCTGGATTCCAGGCCTAGGTCTTCTGTTCTGTTCTCTATAAAATGTTGC
CATAGTGCCTGTGCTGATTGACAACACCAAGCGGTTCTATTCTCTTCTGTTGT
AGGAGAAGTTGAAGATGAATTACTCATGCCTACAGCAAAGTGTATACATTAGACATCCC
[T, C]

CTTCTCATGGTTCGCCTGGCAGTCCTGTGGCAGTAACACTAACTGTGCCATTGCTCTC
TTCCCAGTAAGTACATAAGACTTGTGAAAGAAACCTACTTGACCCATAAATTAGTAC

FIGURE 3V



21840

ATGTGTTCTACCTTCATTGGTATTAAATTAGGGTGAGTTGCAATTGCAATGCCCTGAC
GATATTATTTCTATAGCATTGGTACTTAAATTGGCATTAAATGTGAGTAGAG
AGCAAGTAGTTCAGGTGGTATTAAATAGTGTAGGAAAAAAATCATAAAACTTATTTT

SEQ ID NO: 42

AAACAGTTATGCTATCTACATATCTCTCACACATGGCCTGCCAGACTCACACC
AGGTCACCCCCTCCCTGGCATTTGTCTGGTGTGAGTTGAGATCCCAGAGCAGA
GCTGGTAGTGAAGATTGGCTGTGAGTTAAACCACACCTAAGGATAAACACAGGT
CTTCACCCCTCCTGCCAGCTCTGTTCTAAACACTGAATTACTCATTCTTGGGG
GAAAAAAAATAAGTGACACAGTAACCAGCACTGTCCTGGACATAATGTCCTACAGGGCT
[G, T]
GCATATGAAGACTATTTCTATAATGACACTGTGGTCACTTAAATGAGCTTGTGCTG
AAATATATTGGCACATTCTTTCTATGAGTGCATGAAATCAGATCCGTACTACTATG
GTGGCTAATATTTACTCTAAATCATGTCCTGCCTTAATATATCTGAAAGTATTGAG
ATGACATACACATAGCTTAGCCTAAATCAGCTCGTCTGGTACAAGACAGAAGACA
ACTATAAACAGAAGGTATAAGTGTAGGGTAAATTGCCAGGCAAACAACTTCACTGAGAAA

SEQ ID NO: 43

22783

TGAGAAAATAAGCACTGATATAATCTGACCATCAGGAACAGCAATAGTGTGAAACATT
AGATGCCATTAGAACCAAAATTGACCATAGAACAGAGTTAGAAAAATGACTAACTGC
TGTCTTCATTATGTATTTCACTAACATTAGCATTGAAACATTGACATTATC
CTGTCTCACCCTTGCATGTTACATTATATAATCTGTGTAAGTGTCCACTGCCAC
AGAGTCATAAGTCCCTGGACTTGGTGTGACAGTGAAGTGGCACAGAGGGTGAGCTC
[C, T]
GTCGTGCTTGGGAAGAAAATGGCTTCAAATGAATCTGCCTGCTTGAATGTATAA
ACTGCCTTTCTAGCAAAGCATAGACACTCTTCCCTGGTGAATGTGCTACGAATT
AGCTGGGTTGAGGATCTGGCTAAATGAACCAACCTCCCTACATGAAGGATACACAG
AGATGGTGAACAGAGAGTGGTCACTCCGTGAGTGGATCTCAATCAAGTCTGAGCTA
AATTCAATTCTTACTAAATGATAAAAGTTGTTATTGGCCTTGTCTGTTT

SEQ ID NO: 44

22787

AAATAAACACTGATATAATCTGACCATCAGGAACAGCAATAGTGTGAAACATTAGAT
GCCATTAGAACCAAAATTGACCATAGAACAGAGTTAGAAAAATGACTAACTGCTGTC
CTTCATTATGTATTTCACTAACATTAGCATTGAAACATTGACATTATCCTGT
CCTCACCCCTTGCATGTTACATTATATAATCTGTGTAAGTGTCCACTGCCACAGAG
TCATAAGTCCCTGGACTTGGTGTGACAGTGAAGTGGCACAGAGGGTGAGCTCTGTC
[G, A]
TGCTTGGGAAGAAAATGGCTTCAAATGAATCTGCCTGCTTGAATGTATAAACTG
CTTTCTAGCAAAGCATAGACACTCTTCCCTGGTGAATGTGCTACGAATTAGCT
GGGTTGAGGATCTGGCTAAATGAACCAACCTCCCTACATGAAGGATACACAGAGAT
GGTGACAGAGAGTGGTCACTCCGTGAGTGGATCTCAATCAAGTCTGAGCTAAATT
CAATTCTTACTAAATGATAAAAGTTGTTATTGGCCTTGTCTGTTT

SEQ ID NO: 45

22825

CAATAGTGTAAACATTAGATGCCATTAGAACCAAAATTGACCATAGAACAGAGTT
AGAAAAATGACTAACTGCTGCTTCAATTATGTATTTCACTAACATTAGCATTATGA
AACATTTCGACATTATCCTGCTCCTACCCCTTGCATGTTACATTATATAATCTGTGTA
AGTGCTCCACTGCCACAGAGTCATAAGTCCCTGGACTTGGTGTGACAGTGA
GGCACAGAGGGTGAGCTGTCGTGCTTGGGAAGAAAATGGCTTCAAATGAATCTG
[T, C]
TTGTCTTGAATGTATAAACTGCCTTTCTAGCAAAGCATAGACACTCTTCCCTGGT
GACATGTGCTACGAATTAGCTGGTTGAGGATCTGGCTAAATGAACCAACCTCC
TACATGAAGGATACACAGAGATGGTGAAGAGAGTGGTCACTCCGTGAGTGGATCTCAA
TCAAGTCTCTGAAGCTAAATTCAATTCTTACTAAATGATAAAAGTTGTTAT
TGGCCTTGTGTTATTCTGATAACTTAGGGTCAGATTCAATGTGTC
SEQ ID NO: 46

22967

CCTCACCCCTTGCATGTTACATTATATAATCTGTGTAAGTGTCCACTGCCACAGAG
TCATAAGTCCCTGGACTTGGTGTGACAGTGAAGTGGCACAGAGGGTGAGCTGTC

FIGURE 3W



23248	CATGAAGGATACACAGAGATGGTGCACAGAGAGTGGTCACTTCCGTGAGTGATCTCAATC AAGTCCTCTGAAGCTAAATTCAATTTCCTTACTAAAATGATAAAAGTTGTTATTG GCGCTTTGCTTGTATTCGTATAACTTAGGGCTCAGATTTCAATGTCATAATGCT GACTCACAGCATGGTCTCTGACAGTTATTCACTTAAGGAACCTTCACCACTGAAGT TTATTTACTTGCTTGATATCTCACACATTAATAATAAAAACAAACAAACCTAATCTGA [A,G] TTAAAATCTATCAGCTTAGGCATTATTTGTGTTCTCCTCTTCAACATGGTAACGG GCTCTCTTCTAGGAGCTTGAGAAGATATGACTGGGGTTGTTCTACTTCATT ATTATCTTCTTCTTCCAATCAGGTTAGTTCTTCTTCTTACTAAAAGGTGCATAGTA ACTGCTTGTAGTATTGTTGAACAAGTGAATAAAATGAAATTAAAGGTAGTGTCTTCA CTAGCAGCCCCAACATTCTTCTCTTAGTAGTGGTGGGTATCAGTTATGGAATGGC SEQ ID NO: 48
23764	GAAATGAATTAAAGGTAGTGTCTTCACTAGCAGCCCCAACATTCTTCTCTTAGTAGTGT GGTGGGGTATCAGTTATGGAATGGCACCTCCTCCAGAGGACTGATCATGTCATTCTCAG CTTATGCTCCCTTATGCAGTAAAGTTCCATATTCCATAAAAGAACAAAGAACCAAAT AATCCAATGGATATATAATGAACACACAGATGAAAATTCCACCTGCCATGCCCTTGA AAAGATCCCTAGCTACTTGTATTCTATCTTATAATTAAATCAGTCTTCACTTATGTT [G,T] TCTTCAGATCTCTGTTTGAAGTGTATATAGATATCAACATAGAAATGCAGCGTATATT GCTATCAACTGCAGTGGAGCAGTGATTGTTCAACATCCTGCCCTTAAAGCAA CCTGAAAATCAAAGTGTGAGCTACGTCTAAACAATGGGAGAGGCTTTTTTTTT AAGAGTTAGAACTAAGACTCTCACTTCTCTGTGCCCTCACATTGACCTTCACATT GGGCCCCCTGCATCAGAATACAGCACCCCCCTAACAGGCTCTGTTCAGGACTCTTCTG SEQ ID NO: 49
23765	AAATGAATTAAAGGTAGTGTCTTCACTAGCAGCCCCAACATTCTTCTCTTAGTAGTGT GTGGGGTATCAGTTATGGAATGGCACCTCCTCCAGAGGACTGATCATGTCATTCTCAG TTATGCTCCCTTATGCAGTAAAGTTCCATATTCCATAAAAGAACAAAGAACCAAATA ATCCAATGGATATATAATGAACACACAGATGAAAATTCCACCTGCCATGCCCTTGA AAAGATCCCTAGCTACTTGTATTCTATCTTATAATTAAATCAGTCTTCACTTATGTT [C,T] CTTCAGATCTCTGTTTGAAGTGTATATAGATATCAACATAGAAATGCAGCGTATATT CTATCAACTGCAGTGGAGCAGTGATTGTTCAACATCCTGCCCTTAAAGCAAAC CTGAAAATCAAAGTGTGAGCTACGTCTAAACAATGGGAGAGGCTTTTTTTTT AAGAGTTAGAACTAAGACTCTCACTTCTCTGTGCCCTCACATTGACCTTCACATTG GGGCCCCCTGCATCAGAATACAGCACCCCCCTAACAGGCTCTGTTCAGGACTCTTCTG SEQ ID NO: 50
24432	GGATGGTGCTGGGGACCTCCCTGACCCACAGCATCTGACCCACATTCCAGGTTCTAGC GACTTGTGTCAGTAAGAAAAAGGCACATAGCTAAGTGGAGAGCAGATGAGGCTTGGTG GGAATCAGCCAGTGGCTGCCCCTAGCAAAGGTAACAGAACACTGCTGGGGCTTTGGTCC TAGGCTCACTACTCAGGGAGGCACTTAACATGGAATGACCAGCAAGTTCTTCTGAT CTTTCCACCAACACCAAGCCTAGTACCTCCCTCCCTTGTCTGCTCTGCTCTTC [A,G] GGAATGCACTGGAAACCCACCTTCAGTTCTGGAAATTTCCTATTCTTATTCAAGAAA GAGGAAGAAGCTTTGCATTACTCCAACCGTTCTACCTATTCCATATAACCTTCTG SEQ ID NO: 51

FIGURE 3X



24538

TGATCTCATATCATTAGGCCAAATGTTAATCTTCTGGGAGCCAGGAGACTGCTTCACA
TTCAGAGGCCCTGGACATATAGGACTGCCTCACTCACTCACTCAGCTTATTGACTT
GAATGCACCTTTAACAGTGAATAAAAACAAACTGTGAATTCTCTGAAAATGAGC

SEQ ID NO: 51

GATGAGGCTTGGGGAAATCAGCCAGTGGCTGCCCTAGCAAAGGTAACAGAACTGCTG
GGGGCTTTGGCTTAGGCTCACTACTCAGGGAGGCACTTAAACATGGAATGACCGAGCAA
GTTTCTTCTGATCTTCCACCACCAAGCCTAGTACCTCCCTCCCTTTGCT
CTGTTGCTCTTCGGGAATGCACTGGAAACCACTTCAGTTCTGTTGGAAATTTCCTA
TTCCTTATTCAAGAAAGAGGAAGAAGCTTGCATTACTCCAACCGTTCTACCTATTATT
[C, G]
CCATAAACTTCTGTGATCTCATATCATTAGGCCAAATGTTAATCTTCTGGGAGCCAGG
AGACTGCTTCACATTCAAGGCCCTGGACATATAGGACTGCCTCACTCACTCACT
CAGCTTATTGACTTGAATGCACCTTTAACAGTGAATAAAAACAAACTGTGAATT
CTCTGAAAATGAGCCTATATCTCATACTTATTATTCTGTTAACACTGTGAACAAATT
AAGTCCTCTGGCACTATGTATATACCATAAAAAGCTTATTGTAAGCCTACTAATTGGAC

SEQ ID NO: 52

24693

CCTAGTACCTCCCTCCCTTTGCTCTGCTCTTGGGAATGCACTGGAAACCA
TTCAGTTCTGTTGGAAATTCTTCTATTCTTATTCAAGAAAGAGGAAGAAGCTTGCATT
TACTCCAACCGTTCTACCTATTATTCCCATAAAACTTCTGTGATCTCATATCATTAGGCC
AAATGTTAATCTTCTGGGAGCCAGGAGACTGCTTCACATTCAAGGCCCTGGACATAT
AGGACTGCCTCTAACTCACTCACTCAGCTTATTGACTTGAATGCACCTTTAACAG
[T, C]
GACTAAAAAAACAAACTGTGAATTCTGAAATGAGCTATATCTCATACTTATTAT
TCTGTTAACACTGTGAAACAAATTAAAGTCTCTGGCACTATGTATATACCATAAAAAGC
TTATTGTAAGCCTACTAATTGGACCAGTTTGACAATTGAATAAGCACTAATTGAG
ATCATAATGTAGAATTATAGGCTGCTGAGGAAAACAATATCACACCATTGCTTCTCA
GTTTCTTTCAAGATGAGTTCAATGTTCACTAATCCAATTAAAATCCTTACA

SEQ ID NO: 53

24819

AACCGTTCTACCTATTATCCCATAAAACTTCTGTGATCTCATATCATTAGGCCAAATGT
TAATCTTCTGGGAGCCAGGAGACTGCTTCACATTCAAGGCCCTGGACATATAGGACT
GCCTCTAACTCACTCAACTCAGCTTATTGACTTGAATGCACCTTTAACAGTGA
AAAAACAAACTGTGAATTCTCTGAAATGAGCCTATATCTCATACTTATTATTCTGT
TTAACACTGTGAAACAAATTAAAGTCTCTGGCACTATGTATATACCATAAAAAGCTTATT
[C, T]
GTAAGCCTACTAATTGGACCAGTTTGACAATTGAATAAGCACTAATTGAGATCATA
ATGAGAATTATAGGCTGCTGAGGAAAACAATATCACACCATTGCTTCTCAGTTCC
TTTCAAGAATGAGTTCAATGTTCACTAATCCAATTAAAATCCTTACAAGTTA
TTCTTAAACTATTCCAGAGACTATCTGTTGCTATTCTAGAAATGAAATTGCTTCTC
AGCCTAAACAGATGGCTTAATTGGTGGAGTGGATGAAAGGAATGTCACATGAGAA

SEQ ID NO: 54

25743

TATCCAGTTACAGCAGCGTAACCTGAGCAGCTGCTGCAAACCTGAGGCCTCTTGCACCTT
CGCCTACTTATTCTAGCTGCTAAAATAGGGCTGAAATCTGTCAGGATCTGAAGGGAAG
GATAAGATTCCCTACTATTCAATTAAAGCTTATTCAAGTCTTATTCACTGCTGCTGTG
ACACTAAGCTAGAAAGCTGAGGAATGTTAGATTATTAGGCTCTGTTCTGCCATTCA
TAGATTACAATCTATTGATAGGGAGAGCTAAAAGGAGAGAAAGAGGAAGGAGCAAACA
[C, T]
AAAAACGTAAAATTAAAATACCATTTAAAATTATTAAAATGTTAAATACCAT
GAAAATTAAAGGAAAACCTAGATTCAAAAAATTCTTCAAACTTGTGAAATCAAT
TCAGTGCTTGCCTTAATGTCATCCAGTCTGATGAGACATGTTTGATCAACAAGG
GTTTTACTATGTTCTTAATTATGTCCTGCTGTTATCTCTTGACCGAGATTATT
TTAACAAATAATTCTGAAAACCTAAGAAAGTGAAGCATAAAATATTGCTTATAAAAATA

SEQ ID NO: 55

26044

AAAAACGTAAAATTAAAATACCATTTAAAATTATTAAAATGTTAAATACCAT
GAAAATTAAAGGAAAACCTAGATTCAAAAAATTCTTCAAACTTGTGAAATCAAT

FIGURE 3Y



TCAGTGCTGCCCTTAATGTCATCCAGTCTGATGAGACATGTTTGTGATCAACAAG
GTTTACTATGTTCTTAATTATGTGCTTGCTGCTTATCTCTTCTGACCGAGATTATT
TTAACAAATAAATTCTGAAAAGTCAAAGCATAAAATATTGTCTTATAAAATA
[G, C]
GCCAAGGAAAAATGACACTCCATTCAAATATCAAAGTTAGCATCAAGACTGCACAAG
ATGAATGTACAGTCATGTGTTGCTTACAAATGTGGACATATTCTGAGAAATGCATCTTAA
GGCAATTGTCATTGTGCAAACACCAGATTGACTTGCAGCCTAATTGGTGGAGCCT
ACTATACACTAAGGCTATATGGCATAGCCTAGTACTCCTAGGCTACAAACCTGTACAGCA
TGTTACTGTAAGTAGTGGAGGTACCTGTAACATAATGTTAAGTATTGTGCTCCAA

SEQ ID NO: 56

26555 AGTACTCCTAGGCTACAAACCTGTACAGCATGTTACTGTACTGAATAGTGGAGGTACCTG
TAACATAATGTTAAGTATTGTGCTCCAAACGTAGAAAAGCTACTGAAAAATACAGTA
TTACAACCTTAGGGTATCACTGCTTATATGTGGTCTGTTGACCGAAATGACTATGC
TTAATACCACTGAACTGTACACTTAAAATGGTTAAGATGGTAAATTCTATGTTATGTAT
GTTTATAATAATAAAAAAATTGAAAAAGCATCAACATCTTCTGGAAAAAGAAAA
[G, A]
GAAAGAAAATGCATTAGAGTGATGAGAATATTGAAGTAATAGATAAAAGTCAAAACAAA
GAAATGATCTTGCTTTGAACTTCTGTTAAGATTGCTACATCAGTGTACACTGTT
ATTCCCAAACGACCCCTCAGCTGGATACGACATTCTGATTGCACTGTGCTTATTGC
ACTTAATAATGTTCTGGTCATCCTGTGCCAACATAAAATACATCTCGGATTCAAGG
TGAGTTCAAGAAGGCTCAATTGGTCAACCCAAACTCACGCTCATTAAATGATGGAC

SEQ ID NO: 57

27886 GGTTATTTAAAGTGTGCTGGCATCTCCTTGCTAGGAACGTGCTGGTAAGACATTGA
CCTTGCCTGTTGTCTTCTCAGGGGCTTCTCTGCCACTATGCTGATTTTATTCTT
CCAGCAGTTTTATCTTAAACTTGCAAGAAAGAAACTTTAGGTCAACCCAAAAGGTC
GGGGTAAGTAAACCTTGCAATTCCCCCATTATTAGTTGTTCTCCAACACTTAAAGATA
AACTAGAAAATACACATAGTCAGAAAATGAATCAATGTACAAGAACCAAAATCAAAA
[A, C]
TGGGCTAGAACCTCTGGTAGCAGAGAAGGGGACATATTCTGAAACTCAAATGATTCT
ACTTCAAATATCAAATATCCTGTGTTGAGTCTGTACATGTCAAATAGTAGTAGCCTT
TCCCACAGACACATATGCTCAGGCAAATAGCAGTGTCCAATACCAAGCTGCTTGTG
TATCCGTGGAAAATCATGCAAGAAGGAATTAGGCTCCCTAGCGGTGTTATGGAATAATT
AAATATTGGTCAAGGCAAAGGAAAGATGTTGTTATTGTT

SEQ ID NO: 58

31884 CTTTATGGTTAGTTGAAAGAATCCATTGAAGATAGAAAATGAGAGAATAGAAGAAAACC
TGAGAATAGAAAATAAGAGCAGAGAAAATATGGGGCAGGGAAAACATGTGAGTGT
AGGATTGATTATGAATGAACGATTAGGGGATTGATGGATCACAGGGTAAGTATATGCTT
AACTTTATAAGAAAATTCCACATAGTTTCCACAGTGTGTTCTACCATTTCAATTCCACC
CGTACTACCTACAACCTCCACTGACTCCACAGCCCTGCCAACATTGGTGTCTTTG
[T, C]
ATTTAGCCTTCTAGTGGCTGAAATGGTAACTCATTGTGATTTCATTCTGCTTCT
GTGACAACATAATGTTAAAACCTTCAAGTGTGTTAATGGTCACTCATATATCTCTTTG
TGAAGTGTGATTCAAATCTTGTGCCATTAAAATTAGGTATGTGTTTTATTGG
GTATTGGTAGAAGCTTTAAATATGGATCCATGTCCAGATTGCCAATATATTCCAG
TCTATGGTATGGTGTCTTATTCTAAAGGTGCTTAATTACATCTTCTGGGCCAGG

SEQ ID NO: 59

32229 TTTCATTCTGCTTCTGTGACAACATAATGTTGAAAACCTTCAAGTGTGTTAATGGTC
CATATATCTTCTTGTGAAAGTGTGATTCAAATCTTGTGCCATTAAAATTAGGT
TATGTGTTTTATTGGTATTTGAGAAGCTTTAAATATGGATCCATGTCCAGATTGC
CAATATATTCCAGTCTATGGTATGGTGTCTTATTCTCAAAGGTGCTTAATTACA
TCTTCTGGGCCAGGTACCCATAGCTAAAGTTGCAATTATGTCTTAATGAGATAA
[T, A]
ATTAATCAGAGTGGTATAGTCAAAATTAAATGTTGATGTGCTGGCCCATAGGTAG
GACTGGATCATCTAACCAAGATGCAAAAAAAAAACAAAAAAGAAAAATGACTTG

FIGURE 3Z

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Inventor: Karl GUEGLER et al.

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FIGURE 3AA